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(54) Title: MATERIALS AND METHODS FOR THE MODIFICATION OF PLANT CELL WALL POLYSACCHARIDES

(57) Abstract

Novel isolated polynucleotides and polypeptides associated with the synthesis of plant cell wall polysaccharides are provided, together with genetic constructs comprising such sequences. Methods for using such constructs for the modulation of polysaccharide content in plants are also disclosed, together with transgenic plants comprising such constructs.

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# MATERIALS AND METHODS FOR THE MODIFICATION OF PLANT CELL WALL POLYSACCHARIDES

## 5 Technical Field of the Invention

This invention relates to the field of modification of cell wall polysaccharide content and composition in plants. More particularly, this invention relates to enzymes involved in the synthesis of plant cell wall polysaccharides and nucleotide sequences encoding such enzymes.

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#### Background of the Invention

Plant cells are characterised by having a rigid cell wall. These cell walls are comprised primarily of polymers of simple sugar monomers linked in a variety of linear or branched polymers known as polysaccharides. The most abundant simple sugar monomer is glucose, and the most abundant polymer is cellulose. Cellulose is a linear, unbranched polymer, comprised of  $\beta$ -1,4 linked glucose monomers. Other polysaccharides found in plant cell walls include hemicellulose, which is a group of polysaccharides comprised of  $\beta$ -1,4 linked glucose monomers having side chains which may include sugars other than glucose. These side chains frequently include xylose, fucose, arabinose, and galactose. Pectins are another type of polysaccharide found in plant cell walls. Pectins are acidic polysaccharides, which are generally comprised primarily of galacturonic acid and rhamnose sugar monomers. Amylose is an additional common plant polysaccharide which is not usually found as a major component of cell walls. It acts primarily as a storage material for glucose, rather than as a structural polymer. However, because amylose is comprised primarily of  $\alpha$ -1,4-linked glucose monomers, it is considered to be a related polymer from a biochemical and physiological perspective.

Plant polysaccharides have many uses. Certain plastics, such as cellulose acetate, and synthetic textiles, such as rayon, are made from cellulose. In addition, some biodegradable plastics and digestible medicine capsules, as well as medical fillers and fiber additives for food, can be made from plant polysaccharides.

In foodstuffs, polysaccharides have a profound impact on food quality. Cell walls contribute to crispness in carrots, while degradation of cell walls is required for softening of fruits, such as peaches and tomatoes. In maize, increased amylose is desirable for cattle feed, but not for human consumption, and increased cell wall strength reduces digestibility. In fiber crops, such as timber, cellulose is the primary polymer of interest. Wood density, a fundamental measure of structural timber quality, is essentially a measure of cellulose content. In the paper pulping industry, efficiency is measured in terms of yield of cellulose. Clearly, the ability to increase cellulose content in timber is an important economic goal.

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The sugars which make up plant cell wall polysaccharides are produced in the photosynthetic organs of plants. The sugars so produced are commonly converted into sucrose, a disaccharide consisting of glucose and fructose. Sucrose is transported throughout the plant, to wherever sugar monomers are called for. Thus, the photosynthetic organs are often referred to as a source, while tissues requiring large amounts of sugar monomers are referred to as a sink. Actively growing regions of the plant are generally sink tissues, as new cell wall synthesis requires large amounts of sugar monomers.

When the transported sucrose arrives at the sink destination, it must be converted into whichever kind of sugar monomer is required. The sugar monomers which make up plant cell walls are primarily 5- or 6-carbon sugars. Different sugars are generally distinguished by stereospecific orientation of hydroxyl groups. Plants contain a variety of enzymes, such as isomerases or epimerases, which can rapidly change the orientation of these hydroxyls. In addition, there are a number of enzymes which can add or remove a single carbon from a sugar monomer. The result is a single pool of sugar monomers which the plant can freely inter-convert into whichever kind is needed for cell wall synthesis.

Plant polysaccharides are thus biochemically and physiologically inter-related. All polymers compete for the same pool of sugar monomers, and all sugar monomers can be freely interconverted to other types. Degradation of any one polymer will provide building material for any other. Attempts to engineer changes in one polymer may therefore have pleiotropic effects on other polymers.

The rate of cell wall synthesis is dependent on both the availability of sugar monomers to serve as building blocks for the polymers of the wall, and the enzymes which polymerise those building blocks into polymers. Enzymes which are directly responsible for the

synthesis of the major cell wall polymers, such as cellulose, hemicellulose and pectin, may have a profound impact on the rate of cell wall synthesis. Source-sink relations may play an important role in limiting cell wall synthesis, if the availability of substrates becomes limiting. Polymer degrading enzymes may liberate sugar monomers from unnecessary polymers for use in building new, desired polymers. Enzymes which can isomerise sugars from one form into another can convert the sugars into whichever kind is needed. Each of the different types of cell wall polysaccharides effectively competes for the same pool of sugar monomers, and each represents a potential source of monomers for any of the other polymers.

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The final committed steps in cellulose biosynthesis involve a relatively small number of enzymes. Cellulose synthase (CEL) is believed to function as part of a large, membrane-bound complex which also includes sucrose synthase (SUS: Amor et al., *Proc. Natl. Acad. Sci USA* 92:9353-9357, 1995) and annexin (ANX: Clark and Roux, *Plant Phys.* 109:1133-1139, 1995). This enzyme complex polymerises activated glucose into the cellulose polymer. The glucose is activated by UDP-glucose pyrophosphorylase (UGP), also known as UTP-glucose-1-phosphate uridylyltransferase. These enzymes are believed to be sufficient for the biosynthesis of cellulose from glucose. Other than these steps, the availability of glucose appears to be the most significant rate-limiting step in cellulose biosynthesis.

Glucose is primarily stored in most plants as amylose. Plants routinely store amylose and degrade it to free up the glucose monomers, as needed. By inhibiting the efficiency of glucose storage, or by increasing the liberation of glucose from amylose, the availability of glucose monomers for cellulose biosynthesis can be increased. The rate-limiting enzyme in the storage of glucose as amylose is ADP-glucose pyrophosphorylase (AGP), also known as ATP-glucose-1-phosphate adenylyltransferase (Iglesias et al., *J. Biol. Chem.* 268:1081-1086, 1993). Conversely, the enzyme most responsible for liberating glucose from amylose is amylase (AMA: Kawagoe and Delmer, *Genetic Engineering* 19:63-87, 1997).

These enzymes clearly will be important in the engineering of economically useful changes in cellulose biosynthesis. In addition, there are many other enzymes which may be useful in influencing plant cell wall polysaccharide biosynthesis. Other enzymes likely to be involved in cellulose biosynthesis include 1,4-β-cellobiohydrolase, β-glucosidase, calnexin, cellobiose epimerase, cellobiose phosphorylase, cellulase A, dextransucrase, invertase, phosphodiesterase, phosphoglucomutase, sucrose phosphate synthase, sucrose phosphorylase,

UDP-glucose 4-epimerase and UDP-glucose dehydrogenase. Enzymes believed to be involved in hemicellulose biosynthesis include β-glucanase, arabinan synthase, GDP-fucose pyrophosphorylase, GDP-mannose pyrophosphorylase, 1,3 and 1,4-β-glucanases, 1,3 and 1,4- $\beta$ -glucosidases, mannose- $\delta$ -phosphate isomerase, nDP-hexose pyrophosphorylase, xyloglucan endotransglycosylase and xyloglucan synthase. Enzymes likely to be involved in pectin biosynthesis include α-galactosidase, β-glucuronidase, exopolygalacturonase, glucuronosyltransferase, pectin methyl-esterase, polygalacturonase and UDP-hexose-1-phosphate uridylyltransferase. Enzymes believed to be involved in amylose biosynthesis include α-glucosidase, amylopectin 6-glucanohydrolase, amylopectin-branching glycosyltransferase,  $\beta$ -amylase, branching enzyme, inulosucrase, isoamylase, isomaltase, levansucrase, starch phosphorylase and starch synthase. Enzymes likely to be involved in the interconversion of 5-carbon sugars include 2-dehydro-3-deoxy-gluconokinase, aldehyde reductase, arabinose isomerase, D-arabinitol dehydrogenase, D-xylulose reductase, endo-1,4-β-xylanase, exo-1,4β-xylanase, L-arabinose isomerase, L-ribulokinase, L-xylulokinase, phospho-ribulokinase, ribose 5-phosphate isomerase, ribulose-phosphate-3-epimerase, ribulose-phosphate-4epimerase, transaldolase, transketolase, xylose isomerase and xylulokinase. Enzymes likely to be involved in interconversion of 6-carbon sugars include 6-phospho-fructo-1-kinase, 6-phospho-fructo-2-kinase, trehalose phosphate synthase, aldolase, aldose 1-epimerase, D-fructokinase, D-galactokinase, fructose 1,6-diphosphatase, gluconolactonase, glucose 1-phosphatase, glucose 6-phosphatase, glucose 6-phosphate dehydrogenase, glucosephosphate isomerase, hexokinase, phosphoglucomutase, trehalase, trehalase phosphatase and UDP-galactose dehydrogenase.

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While DNA sequences encoding some of the enzymes involved in the biosynthetic pathways of plant cell wall polysaccharides have been isolated for certain species of plants, genes encoding many of the enzymes in a wide range of plant species have not yet been identified. Thus, there remains a need in the art for materials useful in the modification of cell wall polysaccharide content and composition in plants.

## Summary of the Invention

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Briefly, the present invention provides polynucleotides isolated from eucalyptus and pine which encode enzymes involved in the synthesis of cell wall polysaccharides. Genetic constructs including such sequences and methods for the use of such constructs are also provided, together with transgenic plants having altered cell wall polysaccharide content and composition.

In one embodiment, the isolated polynucleotides comprise a nucleotide sequence selected from the group consisting of: (a) sequences recited in SEQ ID NOS: 1-29, 57-80, 105, 107, 109-113, 119-129, 139-143 and 149-908; (b) complements of the sequences recited in SEQ ID NOS: 1-29, 57-80, 105, 107, 109-113, 119-129, 139-143 and 149-908; (c) reverse complements of the sequences recited in SEQ ID NOS: 1-29, 57-80, 105, 107, 109-113, 119-129, 139-143 and 149-908; (d) reverse sequences of the sequences recited in SEQ ID NOS: 1-29, 57-80, 105, 107, 109-113, 119-129, 139-143 and 149-908; and (e) sequences having either 40%, 60%, 75% or 90% identical nucleotides, as defined herein, to a sequence of (a) – (d).

In a further aspect, isolated polypeptides encoded by a polynucleotide of the present invention are provided. In one embodiment, such polypeptides comprise an amino acid sequence selected from the group consisting of SEQ ID NOS: 30-56, 81-104, 106, 108, 114-118, 129-138 and 144-148, and variants thereof.

In another aspect, the invention provides genetic constructs comprising a polynucleotide of the present invention, either alone, in combination with one or more of the inventive polynucleotide sequences, or in combination with one or more known polynucleotides, together with transgenic cells comprising such constructs.

In a related aspect, the present invention provides genetic constructs comprising, in the 5'-3' direction, a gene promoter sequence; an open reading frame coding for at least a functional portion of an enzyme encoded by a polynucleotide of the present invention or a variant thereof; and a gene termination sequence. The open reading frame may be orientated in either a sense or antisense direction. Genetic constructs comprising a non-coding region of a gene coding for an enzyme encoded by the above polynucleotides or a nucleotide sequence complementary to a non-coding region, together with a gene promoter sequence and a gene termination sequence, are also provided. Preferably, the gene promoter and termination

sequences are functional in a host plant. Most preferably, the gene promoter and termination sequences are those of the original enzyme genes but others generally used in the art, such as the Cauliflower Mosaic Virus (CMV) promoter, with or without enhancers such as the Kozak sequence or Omega enhancer, and *Agrobacterium tumefaciens* nopalin synthase terminator may be usefully employed in the present invention. Tissue-specific promoters may be employed in order to target expression to one or more desired tissues. In a preferred embodiment, the gene promoter sequence provides for transcription in xylem. The genetic construct may further include a marker for the identification of transformed cells.

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In a further aspect, transgenic plant cells comprising the genetic constructs of the present invention are provided, together with plants comprising such transgenic cells, and fruits, seeds and other products, derivatives, or progeny of such forestry plants. Propagules of the transgenic plants transformed with the inventive polynucleotides are also included in the present invention. As used herein, the word "propagule" means any part of a plant that may be used in reproduction or propagation, sexual or asexual, including cuttings.

Plant varieties, particularly registrable plant varieties according to Plant Breeders' Rights, may be excluded from the present invention. A plant need not be considered a "plant variety" simply because it contains stably within its genome a transgene, introduced into a cell of the plant or an ancestor thereof.

In yet another aspect, methods for modulating the polysaccharide content and composition of an organism, such as a plant, are provided, such methods including stably incorporating into the genome of the plant a genetic construct of the present invention. In a preferred embodiment, the target plant is a woody plant, preferably selected from the group consisting of eucalyptus, pine, acacia, poplar, sweetgum, teak and mahogany species, more preferably from the group consisting of pine and eucalyptus species, and most preferably from the group consisting of Eucalyptus grandis and Pinus radiata. In a related aspect, a method for producing a plant having modified cellulose content is provided, the method comprising transforming a plant cell with a genetic construct of the present invention to provide a transgenic cell and cultivating the transgenic cell under conditions conducive to regeneration and mature plant growth.

In yet a further aspect, the present invention provides methods for modifying the activity of a polypeptide in a plant, comprising stably incorporating into the genome of the

plant a genetic construct of the present invention. In a preferred embodiment, the target plant is a woody plant, preferably selected from the group consisting of eucalyptus, pine, acacia, poplar, sweetgum, teak and mahogany species, more preferably from the group consisting of pine and eucalyptus species, and most preferably from the group consisting of *Eucalyptus grandis* and *Pinus radiata*.

The above-mentioned and additional features of the present invention and the manner of obtaining them will become apparent, and the invention will be best understood by reference to the following more detailed description. All references disclosed herein are hereby incorporated by reference in their entirety as if each was incorporated individually.

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## Brief Description of the Figures

Fig. 1 illustrates the level of native CEL enzyme activity in positive control mung bean (V. radiata) plants.

Fig. 2 illustrates the level of CEL enzyme activity in mammalian 293T cells transfected with *E. grandis* CEL as compared to that in non-transfected 293T cells.

## **Detailed Description**

As outlined above, cellulose is formed by polymerization of glucose into a linear, unbranched, polymer comprised of  $\beta$ -1,4 linked glucose monomers (Kawagoe and Delmer, Genetic Engineering, 19:63-87, 1997). Cellulose is the most important plant cell wall polysaccharide from both a structural, as well as industrial, perspective. Other polysaccharides are essential for healthy cell walls, as well as for many alternative industrial uses.

Glucose monomers are most commonly stored in the plant in the form of amylose by the action of several enzymes, with the rate limiting step for storage being catalysed by AGP (Iglesias et al., *J. Biol. Chem.* 268:1081-1086). Glucose monomers are freed from this storage polymer by the action of the enzyme AMA. The free monomers are activated by the action of the enzyme UGP, and polymerised into cellulose macro-crystalline structures by the action of the cellulose synthase enzyme complex. Pure CEL enzyme has been shown to form  $\beta$ -1,4 glucose linkages *in vitro*, but has not been shown to be sufficient for polymerization of the

large polymers which are fundamental to the structure of plant cell walls. The holoenzyme complex appears to be necessary for this latter function. The holoenzyme is believed to be comprised of the CEL enzyme in combination with the SUS enzyme and ANX, the whole complex being integrated into the plasma membrane and forming a "rosette" structure as seen in electron micrographs of plant cell membranes (Arioli et al., *Science* 279:717-720, 1998).

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Because cellulose synthesis can represent such a large sink for sugar monomers in the cell, changes in the rate of cellulose synthesis can have a profound influence on the synthesis of other plant polysaccharides. Conversely, changes in the rates of synthesis of other plant polysaccharides can have a profound influence on the pool of sugars available for synthesis of cellulose. Hence, changes in the synthesis of any single polymer may affect both the content and composition of plant cell wall polysaccharides, and polysaccharides in general.

Quantitative and qualitative modifications in plant polysaccharide content are known to be induced by external factors such as light stimulation, low calcium levels, and mechanical stress. Synthesis of cell wall polysaccharides can also be induced by infection with pathogens.

Using the methods and materials of the present invention, the polysaccharide content of a plant may be increased or reduced, by incorporating additional copies of genes encoding enzymes involved in the synthesis of cell wall polysaccharides into the genome of the target plant. Similarly, an increase or decrease in polysaccharide content may be obtained by transforming the target plant with antisense copies of such genes. In addition, the number of copies of genes encoding for different enzymes in the biosynthetic pathway of cell wall polysaccharides can be manipulated to modify the relative amount of each monosaccharide synthesized, thereby leading to the formation of cell walls having altered composition. The alteration of polysaccharide composition would be advantageous, for example, in tree processing for paper.

The polynucleotides of the present invention were isolated from forestry plant sources, namely from *Eucalyptus grandis* and *Pinus radiata*, but they may alternatively be synthesized using conventional synthesis techniques. Specifically, isolated polynucleotides of the present invention include polynucleotides comprising a sequence selected from the group consisting of sequences identified as SEQ ID NOS: 1-29, 57-80, 105, 107, 109-113, 119-129, 139-143 and 149-908; complements of the sequences identified as SEQ ID NOS: 1-29, 57-80, 105,

107, 109-113, 119-129, 139-143 and 149-908; reverse complements of the sequences identified as SEQ ID NOS: 1-29, 57-80, 105, 107, 109-113, 119-129, 139-143 and 149-908; at least a specified number of contiguous residues (x-mers) of any of the above-mentioned polynucleotides; extended sequences corresponding to any of the above polynucleotides; and variants of any of the above polynucleotides, as that term is described in this specification.

In another embodiment, the present invention provides isolated polypeptides encoded by the DNA sequences of SEQ ID NOS: 1-29, 57-80, 105, 107, 109-113, 119-129, 139-143 and 149-908;. The predicted amino acid sequences encoded by SEQ ID NOS: 1-22, 24-28, 57-80, 105, 107, 109-113 and 119-143, based on the best available information at the time of filing this application, are provided in SEQ ID NOS: 30-56, 81-104, 106, 108, 114-118, 129-138 and 144-148, respectively. The present invention also encompasses polynucleotides that differ from the disclosed sequences but which, due to the degeneracy of the genetic code, encode a polypeptide which is the same as that encoded by a polypeptide of the present invention. Such polynucleotides are said to be "degeneratively equivalent" to a polynucleotide sequence disclosed herein.

The polynucleotides and polypeptides of the present invention were putatively identified by DNA and polypeptide similarity searches. In the attached Sequence Listing SEQ ID NOS: 1-29, 57-80, 105, 107, 109-113, 119-129, 139-143 and 149-908 are polynucleotide sequences, and SEQ ID NOS: 30-56, 81-104, 106, 108, 114-118, 129-138 and 144-148 are polypeptide sequences. The polynucleotides and polypeptides of the present invention, have demonstrated similarity to enzymes that are known to be involved in the synthesis of cell wall polysaccharides. The putative identity of each of the inventive polynucleotides is shown below in Table 1.

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TABLE 1

DNA SEQ ID NO:	PROTEIN SEQ ID NO:	IDENTITY	
1	30	AGP	
2	31	AGP	
3	32	AGP	
4	33	AMA	

DNA SEQ ID NO:	PROTEIN SEQ ID NO:	IDENTITY
5	34	AMA
6	35	AMA
7	36	CEL
8	37	CEL
9	38	CEL
10	39	CEL
11	40	CEL
12	41	CEL
13	42	CEL
14	43	CEL
15	44	SUS
16	45	SUS
17	46	SUS
18	47	SUS
19	48	SUS
20	49	UGP
21	50	UGP
22	51	UGP
23	-	UGP
24	52	ANX
25	53	ANX
26	54	ANX
27	55	ANX
28	56	ANX
29	-	ANX
57	81	AMA
58	82	AMA
59	83	AGP
60	84	AGP
61	85	AGP
62	86	AGP
63	87	AGP
64	88	AGP
65	89	AGP
66	90	CEL
67	91	CEL
68	92	CEL
69	93	CEL
70	94	CEL
71	95	SUS
72	96	SUS
73	97	SUS
74	98	SUS
75	99	SUS
76	100	SUS
77	101	SUS
78	102	SUS
79	103	UGP
80	104	UGP

DNA SEQ ID NO:	PROTEIN SEQ ID NO:	IDENTITY	
105	106	SUS	
107	108	CEL	
109	114	ANX	
110	115	ANX	
111	116	ANX	
112	117	ANX	
113	118	ANX	
119	129	CEL	
120	130	CEL	
121	131	CEL	
122	132	CEL	
123	133	CEL	
124	134	CEL	
125	135	CEL	
126	136	CEL	
127	137	CEL	
128	138	CEL	
135	144	SUS	
140	145	α-amylase	
141	146	CEL	
142	147	AGP (3' end of SEQ ID NO: 62)	
143	148	SUS (3' of SEQ ID NO: 74)	
149-185	•	1,3-β-D-Glucanase	
		1,4-β-Cellobiohydrolase	
187-196			
197-204	-	α-glucosidase	
205-250	•	aldolase	
251	-	Amylopectin 6-glucanohydrolase	
252-262	-	β-amylase	
263	•	β-glucosidase	
264-272	-	Branching enzyme	
273-318	-	D-fructokinase	
319-354	•	D-xylulose reductase	
355-365	-	Endo-1,3-1,4-β-glucanase	
366-371	-	Glucan exo-1,3-β-glucosidase	
372-377	-	Glucose 6-phosphate dehydrogenase	
378-381	-	Glucose phosphate isomerase	
382-389	•	Isoamylase	
390-393	•	L-ribulokinase	
394-398			
399-478	399-478 - Pectin methyl-esterase		
479-506	-	Phosphoglucomutase	
507-508	-	Phospho-ribulokinase	
509-521	•	Ribulose-phosphate-3-epimerase	
522-530	•	Starch phosphorylase	
531-551	-	Sucrose phosphate synthase	
552-555	•	SUS	
556-586	-	Transketolase	
587-591	587-591 - Trehalase		

		PROTEIN SEQ ID NO:	IDENTITY
		-	UDP-glucose 4-epimerase
		<u>-</u>	Xyloglucan endotransglycosylase
	903-908	<u>-</u>	Xylose isomerase

The term "polynucleotide(s)," as used herein, means a single or double-stranded polymer of deoxyribonucleotide or ribonucleotide bases and includes DNA and corresponding RNA molecules, including HnRNA and mRNA molecules, both sense and anti-sense strands, and comprehends cDNA, genomic DNA and recombinant DNA, as well as wholly or partially synthesized polynucleotides. An HnRNA molecule contains introns and corresponds to a DNA molecule in a generally one-to-one manner. An mRNA molecule corresponds to an HnRNA and DNA molecule from which the introns have been excised. A polynucleotide may consist of an entire gene, or any portion thereof. Operable anti-sense polynucleotides may comprise a fragment of the corresponding polynucleotide, and the definition of "polynucleotide" therefore includes all such operable anti-sense fragments.

The term "polypeptide", as used herein, encompasses amino acid chains of any length including full length proteins, wherein amino acid residues are linked by covalent peptide bonds. Polypeptides of the present invention may be naturally purified products, or may be produced partially or wholly using recombinant techniques.

The definition of the terms "complement", "reverse complement" and "reverse sequence", as used herein, is best illustrated by the following example. For the sequence 5' AGGACC 3', the complement, reverse complement and reverse sequence are as follows:

20 complement 3' TCCTGG 5' reverse complement 3' GGTCCT 5'

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reverse sequence 5' CCAGGA 3'.

As used herein, the term "variant" covers any sequence which has at least about 40%, more preferably at least about 60%, more preferably yet at least about 75% and most preferably at least about 90% identical residues (either nucleotides or amino acids) to a sequence of the present invention. The percentage of identical residues is determined by aligning the two sequences to be compared, determining the number of identical residues in

the aligned portion, dividing that number by the total length of the inventive, or queried, sequence and multiplying the result by 100.

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Polynucleotide or polypeptide sequences may be aligned, and percentage of identical nucleotides in a specified region may be determined against another polynucleotide, using computer algorithms that are publicly available. Two exemplary algorithms for aligning and identifying the similarity of polynucleotide sequences are the BLASTN and FASTA algorithms. The similarity of polypeptide sequences may be examined using the BLASTP algorithm. Both the BLASTN and BLASTP software are available on the NCBI anonymous FTP server (ftp://ncbi.nlm.nih.gov) under /blast/executables/. The BLASTN algorithm Version 2.0.6 [Sept-16-1998], set to the default parameters described in the documentation and distributed with the algorithm, is preferred for use in the determination of variants according to the present invention. The use of the BLAST family of algorithms, including BLASTN and BLASTP, is described at NCBI's Internet website at the URL http://www.ncbi.nlm.nih.gov/BLAST/newblast.html and in the publication of Altschul, Stephen F, et al., "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs," Nucleic Acids Res. 25:3389-3402, 1997. The computer algorithm FASTA is available on the Internet at the ftp site ftp://ftp.virginia.edu/pub/fasta/. Version 2.04, [February 1996], set to the default parameters described in the documentation and distributed with the algorithm, is preferred for use in the determination of variants according to the present invention. The use of the FASTA algorithm is described in Pearson WR and Lipman DJ, "Improved Tools for Biological Sequence Analysis," Proc. Natl. Acad. Sci. USA 85:2444-2448, 1988; and Pearson WR, "Rapid and Sensitive Sequence Comparison with FASTP and FASTA," Methods in Enzymol. 183:63-98, 1990.

The following running parameters are preferred for determination of alignments and identities using BLASTN that contribute to the E values and percentage identity of polynucleotides of the present invention: Unix running command: blastall -p blastn -d embldb -e 10 -G 0 -E 0 -r 1 -v 30-b 30 -i queryseq -o results; and the parameters are: -p Program Name [String]; -d Database [String]; -e Expectation value (E) [Real]; -G Cost to open a gap (zero invokes default behavior) [Integer]; -E Cost to extend a gap (zero invokes default behavior) [Integer]; -r Reward for a nucleotide match (blastn only) [Integer]; -v Number of

one-line descriptions (V) [Integer]; -b Number of alignments to show (B) [Integer]; -i Query File [File In]; -o BLAST report Output File [File Out] Optional.

The following running parameters are preferred for determination of alignments and identities using BLASTP that contribute to the E values and percentage identity of polypeptide sequences: For BLASTP the following running parameters are preferred: blastall –p blastp –d swissprotdb –e 10 –G 0 –E 0 –v 30 –b 30 –i queryseq –o results; and parameters are: -p Program Name [String]; -d Database [String]; -e Expectation value (E) [Real]; -G Cost to open a gap (zero invokes default behavior) [Integer]; -E Cost to extend a gap (zero invokes default behavior) [Integer]; -v Number of one-line descriptions (v) [Integer]; -b Number of alignments to show (b) [Integer]; -I Query File [File In]; -o BLAST report Output File [File Out] Optional.

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The "hits" to one or more database sequences by a queried sequence produced by BLASTN, BLASTP, FASTA, or a similar algorithm, align and identify similar portions of sequences. The hits are arranged in order of the degree of similarity and the length of sequence overlap. Hits to a database sequence generally represent an overlap over only a fraction of the sequence length of the queried sequence.

The BLASTN and FASTA algorithms also produce "Expect" values for alignments. The Expect value (E) indicates the number of hits one can "expect" to see over a certain number of contiguous sequences by chance when searching a database of a certain size. The Expect value is used as a significance threshold for determining whether the hit to a database, such as the preferred EMBL database, indicates true similarity. For example, an E value of 0.1 assigned to a hit is interpreted as meaning that in a database of the size of the EMBL database, one might expect to see 0.1 matches over the aligned portion of the sequence with a similar score simply by chance. By this criterion, the aligned and matched portions of the sequences then have a probability of 90% of being the same. For sequences having an E value of 0.01 or less over aligned and matched portions, the probability of finding a match by chance in the EMBL database is 1% or less using the BLASTN or FASTA algorithm.

According to one embodiment, "variant" polynucleotides, with reference to each of the polynucleotides of the present invention, preferably comprise sequences having the same number or fewer nucleic acids than each of the polynucleotides of the present invention and producing an E value of 0.01 or less when compared to the polynucleotide of the present

invention. That is, a variant polynucleotide is any sequence that has at least a 99% probability of being the same as the polynucleotide of the present invention, measured as having an E value of 0.01 or less using the BLASTN or FASTA algorithms set at the default parameters. According to a preferred embodiment, a variant polynucleotide is a sequence having the same number or fewer nucleic acids than a polynucleotide of the present invention that has at least a 99% probability of being the same as the polynucleotide of the present invention, measured as having an E value of 0.01 or less using the BLASTN or FASTA algorithms set at the default parameters.

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Alternatively, variant polynucleotide hybridize to the polynucleotide of the present invention under stringent conditions. As used herein, "stringent conditions" refers to prewashing in a solution of 6X SSC, 0.2% SDS; hybridizing at 65°C, 6X SSC, 0.2% SDS overnight; followed by two washes of 30 minutes each in 1X SSC, 0.1% SDS at 65°C and two washes of 30 minutes each in 0.2X SSC, 0.1% SDS at 65°C.

The present invention also encompasses polynucleotides that differ from the disclosed sequences but that, as a consequence of the discrepancy of the genetic code, encode a polypeptide having similar enzymatic activity as a polypeptide encoded by a polynucleotide of the present invention. Thus, polynucleotides comprising sequences that differ from the polynucleotide sequences recited in SEQ ID NOS: 1-29, 57-80, 105, 107, 109-113, 119-129, 139-143 and 149-908, or complements, reverse sequences, or reverse complements of those sequences as a result of conservative substitutions are contemplated by and encompassed within the present invention. Additionally, polynucleotides comprising sequences that differ from the polynucleotide sequences recited in SEQ ID NOS: 1-29, 57-80, 105, 107, 109-113, 119-129, 139-143 and 149-908, or complements, reverse complements, or reverse sequences as a result of deletions and/or insertions totaling less than 10% of the total sequence length are also contemplated by and encompassed within the present invention. Similarly, polypeptides comprising sequences that differ from the polypeptide sequences recited in SEQ ID NOS: 30-56, 81-104, 106, 108, 114-118, 129-138 and 144-148 as a result of amino acid substitutions, insertions, and/or deletions totaling less than 10% of the total sequence length are contemplated by an encompassed within the present invention, provided the variant polypeptide has activity in a cell wall polysaccharide synthesis pathway.

Variants of the polypeptide sequences recited in SEQ ID NOS: 30-56, 81-104, 106, 108, 114-118, 129-138 and 144-148, wherein the variant has an activity level that is different to that of the recited polypeptide are also encompassed by the present invention. In specific embodiments, variants of the inventive sucrose synthase (SUS) polypeptides are provided wherein the N-terminal serine phosphorylation site has been replaced by an acidic amino acid (such as Asp or Glu) by, for example, site directed mutagenesis. Nakai et al. have demonstrated that SUS polypeptides mutated in this manner possess increased activity compared to wild-type SUS (Nakai et al., *Plant Cell Physiol.* 39:1337-1341, 1998). Polynucleotides encoding such variants of the inventive SUS polypeptides may therefore be employed in transgenic plants to increase cellulose production.

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The polynucleotides of the present invention may be isolated from various libraries, or may be synthesized using techniques that are well known in the art. The polynucleotides may be synthesized, for example, using automated oligonucleotide synthesizers (e.g., Beckman Oligo 1000M DNA Synthesizer) to obtain polynucleotide segments of up to 50 or more nucleic acids. A plurality of such polynucleotide segments may then be ligated using standard DNA manipulation techniques that are well known in the art of molecular biology. One conventional and exemplary polynucleotide synthesis technique involves synthesis of a single stranded polynucleotide segment having, for example, 80 nucleic acids, and hybridizing that segment to a synthesized complementary 85 nucleic acid segment to produce a 5 nucleotide overhang. The next segment may then be synthesized in a similar fashion, with a 5 nucleotide overhang on the opposite strand. The "sticky" ends ensure proper ligation when the two portions are hybridized. In this way, a complete polynucleotide of the present invention may be synthesized entirely in vitro.

Some of the polynucleotides identified as SEQ ID NOS: 1-29, 57-80, 105, 107, 109-113, 119-129, 139-143 and 149-908 are referred to as "partial" sequences, in that they do not represent the full coding portion of a gene encoding a naturally occurring polypeptide. The partial polynucleotide sequences disclosed herein may be employed to obtain the corresponding full length genes for various species and organisms by, for example, screening DNA expression libraries using hybridization probes based on the polynucleotides of the present invention, or using PCR amplification with primers based upon the polynucleotides of the present invention. In this way one can, using methods well known in the art, extend a

polynucleotide of the present invention upstream and downstream of the corresponding mRNA, as well as identify the corresponding genomic DNA, including the promoter and enhancer regions, of the complete gene. The present invention thus comprehends isolated polynucleotides comprising a sequence identified in SEQ ID NOS: 1-29, 57-80, 105, 107, 109-113, 119-129, 139-143 and 149-908, or a variant of one of the specified sequences, that encode a functional polypeptide, including full length genes. Such extended polynucleotides may have a length of from about 50 to about 4,000 nucleic acids or base pairs, and preferably have a length of less than about 4,000 nucleic acids or base pairs, more preferably yet a length of less than about 3,000 nucleic acids or base pairs, more preferably yet a length of less than about 2,000 nucleic acids or base pairs. Under some circumstances, extended polynucleotides of the present invention may have a length of less than about 1,800 nucleic acids or base pairs, preferably less than about 1,600 nucleic acids or base pairs, more preferably less than about 1,400 nucleic acids or base pairs, more preferably less than about 1,400 nucleic acids or base pairs, more preferably less than about 1,400 nucleic acids or base pairs, more preferably less than about 1,200 nucleic acids or base pairs, and most preferably less than about 1,000 nucleic acids or base pairs.

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Polynucleotides of the present invention also comprehend polynucleotides comprising at least a specified number of contiguous residues (x-mers) of any of the polynucleotides identified as SEQ ID NOS: 1-29, 57-80, 105, 107, 109-113, 119-129, 139-143 and 149-908, complements, reverse sequences, and reverse complements of such sequences, and their Similarly, polypeptides of the present invention comprehend polypeptides variants. comprising at least a specified number of contiguous residues (x-mers) of any of the polypeptides identified as SEQ ID NOS: 30-56, 81-104, 106, 108, 114-118, 129-138 and 144-148, and their variants. As used herein, the term "x-mer," with reference to a specific value of "x," refers to a sequence comprising at least a specified number ("x") of contiguous residues of any of the polynucleotides identified as SEQ ID NO: 1-29, 57-80, 105, 107, 109-113, 119-129, 139-143 and 149-908, or the polypeptides identified as SEQ ID NOS: 30-56, 81-104, 106, 108, 114-118, 129-138 and 144-148. According to preferred embodiments, the value of x is preferably at least 20; more preferably, at least 40; more preferably yet, at least 60; and most preferably, at least 80. Thus, polynucleotides and polypeptides of the present invention comprise a 20-mer, a 40-mer, a 60-mer, an 80-mer, a 100-mer, a 120-mer, a 150-mer, a 180-mer, a 220-mer, a 250-mer, or a 300-mer, 400-mer,

500-mer or 600-mer of a polynucleotide or polypeptide identified as SEQ ID NOS: 1-908, and variants thereof.

Polynucleotide probes and primers complementary to and/or corresponding to SEQ ID NOS: 1-29, 57-80, 105, 107, 109-113, 119-129, 139-143 and 149-908, and variants of those sequences, are also comprehended by the present invention. Such oligonucleotide probes and primers are substantially complementary to the polynucleotide of interest. As used herein, the term "oligonucleotide" refers to a relatively short segment of a polynucleotide sequence, generally comprising between 6 and 60 nucleotides, and comprehends both probes for use in hybridization assays and primers for use in the amplification of DNA by polymerase chain reaction.

An oligonucleotide probe or primer is described as "corresponding to" a polynucleotide of the present invention, including one of the sequences set out as SEQ ID NOS: 1-29, 57-80, 105, 107, 109-113, 119-129, 139-143 and 149-908, or a variant, if the oligonucleotide probe or primer, or its complement, is contained within one of the sequences set out as SEQ ID NOS: 1-29, 57-80, 105, 107, 109-113, 119-129, 139-143 and 149-908, or a variant of one of the specified sequences.

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Two single stranded sequences are said to be substantially complementary when the nucleotides of one strand, optimally aligned and compared, with the appropriate nucleotide insertions and/or deletions, pair with at least 80%, preferably at least 90% to 95%, and more preferably at least 98% to 100%, of the nucleotides of the other strand. Alternatively, substantial complementarity exists when a first DNA strand will selectively hybridize to a second DNA strand under stringent hybridization conditions. Stringent hybridization conditions for determining complementarity include salt conditions of less than about 1 M, more usually less than about 500 mM, and preferably less than about 200 mM. Hybridization temperatures can be as low as 5°C, but are generally greater than about 22°C, more preferably greater than about 30°C. Longer DNA fragments may require higher hybridization temperatures for specific hybridization. Since the stringency of hybridization may be affected by other factors such as probe composition, presence of organic solvents and extent of base mismatching, the combination of parameters is more important than the absolute measure of any one alone. The DNA from plants or

samples or products containing plant material can be either genomic DNA or DNA derived by preparing cDNA from the RNA present in the sample.

In addition to DNA-DNA hybridization, DNA-RNA or RNA-RNA hybridization assays are also possible. In the first case, the mRNA from expressed genes would then be detected instead of genomic DNA or cDNA derived from mRNA of the sample. In the second case, RNA probes could be used. In addition, artificial analogs of DNA hybridizing specifically to target sequences could also be used.

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In specific embodiments, the oligonucleotide probes and/or primers comprise at least about 6 contiguous residues, more preferably at least about 10 contiguous residues, and most preferably at least about 20 contiguous residues complementary to a polynucleotide sequence of the present invention. Probes and primers of the present invention may be from about 8 to 100 base pairs in length or, preferably from about 10 to 50 base pairs in length or, more preferably from about 15 to 40 base pairs in length. The probes can be easily selected using procedures well known in the art, taking into account DNA-DNA hybridization stringencies, annealing and melting temperatures, and potential for formation of loops and other factors, which are well known in the art. Tools and software suitable for designing probes, and especially suitable for designing PCR primers, are available on the Internet, for example, at URL <a href="http://www.horizonpress.com/pcr/">http://www.horizonpress.com/pcr/</a>. Preferred techniques for designing PCR primers are also disclosed in Dieffenbach CW and Dyksler GS, *PCR primer: a laboratory manual*, CSHL Press: Cold Spring Harbor, NY, 1995.

A plurality of oligonucleotide probes or primers corresponding to a polynucleotide of the present invention may be provided in a kit form. Such kits generally comprise multiple DNA or oligonucleotide probes, each probe being specific for a polynucleotide sequence. Kits of the present invention may comprise one or more probes or primers corresponding to a polynucleotide of the present invention, including a polynucleotide sequence identified in SEQ ID NOS: 1-29, 57-80, 105, 107, 109-113, 119-129, 139-143 and 149-908.

In one embodiment, the present invention provides genetic that include an open reading frame coding for at least a functional portion of a polypeptide encoded by a polynucleotide of the present invention or a variant thereof. As used herein, the "functional portion" of a polypeptide is that portion which contains the active site essential for affecting the metabolic step, *i.e.*, the portion of the molecule that is capable of binding one or more

reactants or is capable of improving or regulating the rate of reaction. The functional portion can be determined by targeted mutagenesis and screening of modified protein products with protocols well known in the art. Normally, the functional portion is 10-20 amino acids, but can be shorter or longer. The active site may be made up of separate portions present on one or more polypeptide chains and will generally exhibit high substrate specificity. The term "polypeptide encoded by a polynucleotide" as used herein, includes polypeptides encoded by a nucleotide sequence which includes the partial isolated DNA sequences of the present invention.

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The open reading frame may be inserted in the genetic construct in a sense or antisense orientation, such that transformation of a target plant with the genetic construct will produce a change in the amount or structure of the polypeptide compared to the wild-type plant. Transformation with a genetic construct comprising an open reading frame in a sense orientation will generally result in modified expression of the selected gene, while transformation with a genetic construct comprising an open reading frame in an antisense orientation also generally results in modified expression of the selected gene. A population of plants transformed with a genetic construct comprising an open reading frame of the present invention in either a sense or antisense orientation may be screened for increased or reduced expression of the gene in question using techniques well known to those of skill in the art, and plants having the desired phenotypes may thus be isolated.

Alternatively, expression of a gene involved in the biosynthesis of polysaccharides may be inhibited by inserting a portion of an open reading frame of the present invention, in either sense or antisense orientation, in the genetic construct. Such portions need not be full-length but preferably comprise at least 25 and more preferably at least 50 residues of a polynucleotide of the present invention. A much longer portion or even the full length polynucleotide corresponding to the complete open reading frame may be employed. The portion of the open reading frame does not need to be precisely the same as the endogenous sequence, provided that there is sufficient sequence similarity to achieve inhibition of the target gene. Thus a sequence derived from one species may be used to inhibit expression of a gene in a different species.

In a second embodiment, the inventive genetic constructs comprise a polynucleotide including a non-coding region of a gene coding for a polypeptide encoded by a polynucleotide

of the present invention, or a polynucleotide sequence complementary to such a non-coding region. Examples of non-coding regions which may be usefully employed in such constructs include introns and 5'-non-coding leader sequences. Transformation of a target plant with such a genetic construct may lead to a reduction in the amount of polysaccharide synthesized by the plant by the process of co-suppression, in a manner similar to that discussed, for example, by Napoli et al. (*Plant Cell* 2:279-290, 1990) and de Carvalho Niebel et al. (*Plant Cell* 7:347-358, 1995).

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Alternatively, regulation of polysaccharide synthesis can be achieved by inserting appropriate sequences or subsequences (e.g., DNA or RNA) in ribozyme constructs (McIntyre CL, Manners JM, *Transgenic Res.* 5(4):257-262, 1996). Ribozymes are synthetic RNA molecules that comprise a hybridizing region complementary to two regions, each of which comprises at least 5 contiguous nucleotides in a mRNA molecule encoded by one of the inventive polynucleotides. Ribozymes possess highly specific endonuclease activity, which autocatalytically cleaves the mRNA.

The genetic constructs of the present invention further comprise a gene promoter sequence and a gene termination sequence, operably linked to the DNA sequence to be transcribed, which control expression of the gene. The gene promoter sequence is generally positioned at the 5' end of the DNA sequence to be transcribed, and is employed to initiate transcription of the DNA sequence. Gene promoter sequences are generally found in the 5' non-coding region of a gene but they may exist downstream of the open reading frame, in introns (Luehrsen KR, *Mol. Gen. Genet. 225*:81-93, 1991) or in the coding region, as for example in a plant defence gene (Douglas et al., *EMBO J. 10*:1767-1775, 1991). When the construct includes an open reading frame in a sense orientation, the gene promoter sequence also initiates translation of the open reading frame. For DNA constructs comprising either an open reading frame in an antisense orientation or a non-coding region, the gene promoter sequence consists only of a transcription initiation site having a RNA polymerase binding site.

A variety of gene promoter sequences which may be usefully employed in the DNA constructs of the present invention are well known in the art. The gene promoter sequence, and also the gene termination sequence, may be endogenous to the target plant host or may be exogenous, provided the promoter is functional in the target host. For example, the promoter and termination sequences may be from other plant species, plant viruses, bacterial plasmids,

and the like. Preferably, gene promoter and termination sequences are from the inventive sequences themselves.

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Factors influencing the choice of promoter include the desired tissue specificity of the construct, and the timing of transcription and translation. For example, constitutive promoters, such as the 35S Cauliflower Mosaic Virus (CaMV 35S) promoter, will affect the activity of the enzyme in all parts of the plant. Use of a tissue specific promoter will result in production of the desired sense or antisense RNA only in the tissue of interest. With genetic constructs employing inducible gene promoter sequences, the rate of RNA polymerase binding and initiation can be modulated by external stimuli, such as light, heat, anaerobic stress, alteration in nutrient conditions and the like. Temporally regulated promoters can be employed to effect modulation of the rate of RNA polymerase binding and initiation at a specific time during development of a transformed cell. Preferably, the original promoters from the enzyme gene in question, or promoters from a specific tissue-targeted gene in the organism to be transformed, such as eucalyptus or pine are used. Other examples of gene promoters which may be usefully employed in the present invention include mannopine synthase (mas), octopine synthase (ocs), and those reviewed by Chua et al. (Science 244:174-181, 1989).

The gene termination sequence, which is located 3' to the DNA sequence to be transcribed, may come from the same gene as the gene promoter sequence or may be from a different gene. Many gene termination sequences known in the art may be usefully employed in the present invention, such as the 3' end of the *Agrobacterium tumefaciens* nopaline synthase gene. However, preferred gene terminator sequences are those from the original enzyme gene or from the target species to be transformed.

The genetic constructs of the present invention may also contain a selection marker that is effective in plant cells, to allow for the detection of transformed cells containing the inventive construct. Such markers, which are well known in the art, typically confer resistance to one or more toxins. One example of such a marker is the NPTII gene whose expression results in resistance to kanamycin or hygromycin, antibiotics which are usually toxic to plant cells at a moderate concentration (Rogers et al., in Weissbach, A and H, eds., Methods for Plant Molecular Biology, Academic Press Inc.: San Diego, CA, 1988). Transformed cells can thus be identified by their ability to grow in media containing the

antibiotic in question. Alternatively, the presence of the desired construct in transformed cells can be determined by means of other techniques well known in the art, such as Southern and Western blots.

A transcription initiation site is additionally included in the genetic construct when the sequence to be transcribed lacks such a site.

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Techniques for operatively linking the components of the inventive genetic constructs are well known in the art and include the use of synthetic linkers containing one or more restriction endonuclease sites as described, for example, by Sambrook et al. (*Molecular cloning: a laboratory manual*, CSHL Press: Cold Spring Harbor, NY, 1989). The genetic construct of the present invention may be linked to a vector having at least one replication system, for example *E. coli*, whereby after each manipulation, the resulting construct can be cloned and sequenced and the correctness of the manipulation determined.

The genetic constructs of the present invention may be used to transform a variety of plants, both monocotyledonous (e.g., grasses, corn, grains, oat, wheat and barley), dicotyledonous (e.g., Arabidopsis, tobacco, legumes, alfalfa, oaks, eucalyptus, maple), and Gymnosperms (e.g., Scots pine; see Aronen, Finnish Forest Res. Papers, Vol. 595, 1996), white spruce (Ellis et al., Biotechnology 11:84-89, 1993), and larch (Huang et al., In Vitro Cell 27:201-207, 1991). In a preferred embodiment, the inventive genetic constructs are employed to transform woody plants, herein defined as a tree or shrub whose stem lives for a number of years and increases in diameter each year by the addition of woody tissue. Preferably the target plant is selected from the group consisting of eucalyptus and pine species, most preferably from the group consisting of Eucalyptus grandis and Pinus radiata. Other species which may be usefully transformed with the DNA constructs of the present invention include, but are not limited to: pines such as Pinus banksiana, Pinus brutia, Pinus caribaea, Pinus clausa, Pinus contorta, Pinus coulteri, Pinus echinata, Pinus eldarica, Pinus ellioti, Pinus jeffreyi, Pinus lambertiana, Pinus monticola, Pinus nigra, Pinus palustrus, Pinus pinaster, Pinus ponderosa, Pinus resinosa, Pinus rigida, Pinus serotina, Pinus strobus, Pinus sylvestris, Pinus taeda, Pinus virginiana; other gymnosperms, such as Abies amabilis, Abies balsamea, Abies concolor, Abies grandis, Abies lasiocarpa, Abies magnifica, Abies procera, Chamaecyparis lawsoniona, Chamaecyparis nootkatensis, Chamaecyparis thyoides, Huniperus virginiana, Larix decidua, Larix laricina, Larix leptolepis, Larix occidentalis,

Larix siberica, Libocedrus decurrens, Picea abies, Picea engelmanni, Picea glauca, Picea mariana, Picea pungens, Picea rubens, Picea sitchensis, Pseudotsuga menziesii. Sequoia gigantea, Sequoia sempervirens, Taxodium distichum, Tsuga canadensis, Tsuga heterophylla. Tsuga mertensiana, Thuja occidentalis, Thuja plicata; and Eucalypts, such as Eucalyptus alba, Eucalyptus bancroftii, Eucalyptus botyroides, Eucalyptus bridgesiana, Eucalyptus calophylla, Eucalyptus camaldulensis, Eucalyptus citriodora, Eucalyptus cladocalyx, Eucalyptus coccifera, Eucalyptus curtisii, Eucalyptus dalrympleana, Eucalyptus deglupta, Eucalyptus delagatensis, Eucalyptus diversicolor, Eucalyptus dunnii, Eucalyptus ficifolia, Eucalyptus globulus, Eucalyptus gomphocephala, Eucalyptus gunnii, Eucalyptus henryi, Eucalyptus laevopinea, Eucalyptus macarthurii, Eucalyptus macrorhyncha, Eucalyptus maculata, Eucalyptus marginata, Eucalyptus megacarpa, Eucalyptus melliodora, Eucalyptus nicholii, Eucalyptus nitens, Eucalyptus nova-anglica, Eucalyptus obliqua, Eucalyptus obtusiflora, Eucalyptus oreades, Eucalyptus pauciflora, Eucalyptus polybractea, Eucalyptus regnans, Eucalyptus resinifera, Eucalyptus robusta, Eucalyptus rudis, Eucalyptus saligna, Eucalyptus sideroxylon, Eucalyptus stuartiana, Eucalyptus tereticornis, Eucalyptus torelliana, Eucalyptus urnigera, Eucalyptus urophylla, Eucalyptus viminalis, Eucalyptus viridis, Eucalyptus wandoo and Eucalyptus youmanni; together with hybrids of the above species.

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As discussed above, transformation of a plant with a genetic construct of the present invention will result in a modification in polysaccharide synthesis in the plant. For example, an increase in the production of cellulose in a plant may be obtained by introducing a genetic construct comprising an open reading frame encoding the enzyme CEL in a sense orientation. Similarly, transformation of a plant with a genetic construct comprising either an open reading frame encoding CEL in an antisense orientation or a non-coding (untranslated) region of a CEL gene will lead to a reduction in the cellulose content of the transformed plant.

Techniques for stably incorporating genetic constructs into the genome of target plants are well known in the art and include *Agrobacterium tumefaciens* mediated introduction, electroporation, protoplast fusion, injection into reproductive organs, injection into immature embryos, high velocity projectile introduction and the like. The choice of technique will depend upon the target plant to be transformed. For example, dicotyledonous plants and certain monocots and gymnosperms may be transformed by *Agrobacterium* Ti plasmid

technology, as described, for example by Bevan (*Nucleic Acids Res.* 12:8711-8721, 1984). Targets for the introduction of the genetic constructs of the present invention include tissues, such as leaf tissue, disseminated cells, protoplasts, seeds, embryos, meristematic regions; cotyledons, hypocotyls, and the like. The preferred method for transforming eucalyptus and pine is a biolistic method using pollen (*see*, for example, Aronen, *Finnish Forest Res. Papers*, 595:53, 1996) or easily regenerable embryonic tissues.

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Once the cells are transformed, cells having the inventive genetic construct incorporated in their genome may be selected by means of a marker, such as the kanamycin resistance marker discussed above. Transgenic cells may then be cultured in an appropriate medium to regenerate whole plants, using techniques well known in the art. In the case of protoplasts, the cell wall is allowed to reform under appropriate osmotic conditions. In the case of seeds or embryos, an appropriate germination or callus initiation medium is employed. For explants, an appropriate regeneration medium is used. Regeneration of plants is well established for many species. For a review of regeneration of forest trees, see Dunstan et al., "Somatic embryogenesis in woody plants," in Thorpe TA, ed., In vitro embryogenesis of plants, (Current Plant Science and Biotechnology in Agriculture), Vol. 20, Chapter 12, pp. 471-540, 1995. Specific protocols for the regeneration of spruce are discussed by Roberts et al., ("Somatic embryogenesis of spruce," in Redenbaugh K, ed., Synseed: applications of synthetic seed to crop improvement, Chapter 23, pp. 427-449, CRC Press: [n.p.], 1993). The resulting transformed plants may be reproduced sexually or asexually, using methods well known in the art, to give successive generations of transgenic plants.

As discussed above, the production of RNA in target plant cells can be controlled by choice of the promoter sequence, or by selecting the number of functional copies or the site of integration of the polynucleotides incorporated into the genome of the target plant host. A target plant may be transformed with more than one genetic construct of the present invention, thereby modulating the activity of more than one cell wall polysaccharide enzyme, affecting enzyme activity in more than one tissue, or affecting enzyme activity at more than one expression time. Similarly, a genetic construct may be assembled containing more than one open reading frame coding for a polypeptide encoded by a polynucleotide of the present invention or more than one non-coding region of a gene coding for such a polypeptide. The polynucleotides of the present inventive may also be employed in combination with other

known sequences encoding polypeptides involved in the synthesis of cell wall polysaccharides. In this manner, it may be possible to modify a biosynthetic pathway of cell wall polysaccharides in a non-woody plant to produce a new type of woody plant.

The following examples are offered by way of illustration and not by way of limitation.

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## Example 1

## Isolation and Characterization of cDNA Clones from Eucalyptus grandis

Eucalyptus grandis cDNA expression libraries (from various tissues, including flowers, leaves, phloem, roots, seeds, shoot buds and xylem) were constructed and screened as follows.

mRNA was extracted from the plant tissue using the protocol of Chang et al. (Plant Molecular Biology Reporter 11:113-116, 1993) with minor modifications. Specifically, samples were dissolved in CPC-RNAXB (100 mM Tris-Cl, pH 8,0; 25 mM EDTA; 2.0 M NaCl; 2%CTAB; 2% PVP and 0.05% Spermidine\*3HCl) and extracted with chloroform:isoamyl alcohol, 24:1. mRNA was precipitated with ethanol and the total RNA preparate was purified using a Poly(A) Quik mRNA Isolation Kit (Stratagene, La Jolla, CA). A cDNA expression library was constructed from the purified mRNA by reverse transcriptase synthesis followed by insertion of the resulting cDNA clones in Lambda ZAP using a ZAP Express cDNA Synthesis Kit (Stratagene), according to the manufacturer's protocol. The resulting cDNAs were packaged using a Gigapack II Packaging Extract (Stratagene) employing 1 μl of sample DNA from the 5 μl ligation mix. Mass excision of the library was done using XL1-Blue MRF' cells and XLOLR cells (Stratagene) with ExAssist helper phage (Stratagene). The excised phagemids were diluted with NZY broth (Gibco BRL, Gaithersburg, MD) and plated out onto LB-kanamycin agar plates containing X-gal and isopropylthio-beta-galactoside (IPTG).

Of the colonies plated and picked for DNA miniprep, 99% contained an insert suitable for sequencing. Positive colonies were cultured in NZY broth with kanamycin and cDNA was purified by means of alkaline lysis and polyethylene glycol (PEG) precipitation. Agarose gel at 1% was used to screen sequencing templates for chromosomal contamination. Dye primer

sequences were prepared using a Turbo Catalyst 800 machine (Perkin Elmer/Applied Biosystems Division, Foster City, CA) according to the manufacturer's protocol.

DNA sequences for positive clones were obtained using a Perkin Elmer/Applied Biosystems Division Prism 377 sequencer. cDNA clones were sequenced first from the 5' end and, in some cases, also from the 3' end. For some clones, internal sequence was obtained using subcloned fragments. Subcloning was performed using standard procedures of restriction mapping and subcloning to pBluescript II SK+ vector.

The determined cDNA sequences are provided in SEQ ID NO: 2, 3, 6, 7, 9, 12-15, 18, 19, 21, 23, 26, 28, 29, 57, 58, 60-66, 71-73, 78, 79, 105, 107, 119-128, 139, 141, 142, 149-161, 186-195, 197, 198, 205-233, 252-256, 264, 273-293, 319-330, 366, 373-377, 382-385, 390-393, 399-434, 479-503, 507-512, 522-528, 531-547, 552-554, 556-573, 587-589, 592-612 and 621-771.

## Example 2

Isolation and Characterization of cDNA Clones from Pinus radiata

## Isolation of cDNA clones by high through-put screening

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Pinus radiata cDNA expression libraries (from various tissues, including cell cultures, fascicle meristems, phloem, pollen sacs, roots, seedlings, shoot buds, strobilus and xylem) were constructed and screened as described above in Example 1. DNA sequence for positive clones was obtained using forward and reverse primers on a Perkin Elmer/Applied Biosystems Division Prism 377 sequencer. The determined cDNA sequences are provided in SEQ ID NO: 1, 4, 5, 8, 10, 11, 16, 17, 20, 22, 24, 25, 27, 59, 67-70, 74-77, 80, 109-113, 140, 143, 162-185, 196, 199-204, 234-251, 257-263, 265-272, 294-318, 331-365, 367-372, 378-381, 386-389, 394-398, 435-481, 504-506, 513-521, 529, 530, 548-551, 555, 574-586, 590, 591, 613-620 and 772-908.

#### Example 3

#### Polynucleotide and Amino Acid Analysis

The determined cDNA sequences described above were compared to and aligned with known sequences in the EMBL database (as updated to May 1999). Specifically, the

polynucleotides identified in SEQ ID NO: 1-29, 57-80, 105, 107, 109-111, 115-125, 135-139 and 145-904 were compared to polynucleotides in the EMBL database using the BLASTN algorithm Version 2.0.6 [Sep-16-1998] set to the following running parameters: Unix running command: blastall –p blastn –d embldb –e 10 –G0 –E0 –r1 –v30 –b30 –i queryseq –o results. Multiple alignments of redundant sequences were used to build up reliable consensus sequences. Based on similarity to known sequences from other plant or non-plant species, the isolated polynucleotides of the present invention identified as SEQ ID NO: 1-29, 57-80, 105, 107, 109-113, 119-129, 139-143 and 149-908 were putatively identified as encoding the enzymes shown in Table 1, above.

The cDNA sequences of SEQ ID NO: 58, 60, 62, 64, 65, 67-70, 72, 74, 75, 77, 78, 80, 105, 107, 119-121, 123-128 and 139-143 were determined to have less than 40% identity to sequences in the EMBL database using the computer algorithm BLASTN, as described above. The cDNA sequences of SEQ ID NO: 57, 59, 66, 79 and 122 were determined to have less than 60% identity to sequences in the EMBL database using BLASTN, as described above. The cDNA sequences of SEQ ID NO: 61, 71, 73 and 76 were determined to have less than 75% identity to sequences in the EMBL database using BLASTN, as described above. The cDNA sequence of SEQ ID NO: 63 was determined to have less than 90% identity to sequences in the EMBL database using BLASTN, as described above.

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#### Example 4

## Functional Identification of Cellulose Biosynthetic Genes

Sense constructs containing sequences including the coding regions for UGP (SEQ ID NO: 23) and SUS (SEQ ID NO: 49) from *Eucalyptus grandis*, and UGP (SEQ ID NO: 24) from *Pinus radiata* were inserted into the expression vector pET16b (Clontech Laboratories Inc, Palo Alto, CA). The resulting constructs were transformed into *E. coli* XL1-Blue (Stratagene) and induced to produce recombinant protein by the addition of IPTG. Purified proteins were obtained using Ni<sup>2+</sup> column chromatography (Janknecht et al., *Proc. Natl. Acad. Sci. USA*, 88:8972-8976, 1991). Enzyme assays for each of the purified proteins demonstrated the expected substrate specificity and enzymatic activity for the genes tested.

Enzyme assays for UGP were performed using published methods (Peng and Chang, FEBS Lett. 329[1,2]:153-158, 1993). The data shown in Table 2 demonstrates enzyme

activity for the expressed proteins as compared to data from Katsube et al. (*Biochem*. 30:8546-8551, 1991) and Nakano et al. (*J. Biochem*. 106:528-532, 1989).

TABLE 2

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SEQ ID NO:	24	23	Katsube et al.	Nakano et al.
Species	P. radiata	E: grandis	S. tuberosum	S. tuberosum
Enzyme	UGP	UGP	UGP	UGP
$\mathbf{K_M}^{G1P}$	0.121	0.126	0.130	0.180
SEM	0.020	0.002	n.a.	n.a.
$\mathbf{K_{M}}^{\mathrm{UTP}}$	0.091	not done	0.076	0.170
SEM	0.015	not done	n.a.	n.a.
K <sub>M</sub> <sup>ATP</sup>	no activity	no activity	no activity	no activity

Enzymé assays for SUS (sucrose synthase) were performed using the methods described by Šebková, V. et al. (*Plant Physiol.*, 108:75-83, 1995). The data shown in Table 3 demonstrates enzyme activity for the expressed proteins. The  $K_M^{Sucrose}$  of *E. grandis* is compared with the data reported by Delmer DP (*J. Biol. Chem.* 247:3822-3828, 1972) and Nakai et al.(*BioSci. Biotech. Biochem.* 61:1500-1503).

TABLE 3

SEQ ID NO:	49	Delmer et al. Nakai et		
Species	E. grandis	V. radiata	V. radiata	
Enzyme	SUS	SUS	SUS	
K <sub>M</sub> Sucrose	1.651	16.700	161.000	
SEM	0.371	n.a.	n.a.	
K <sub>M</sub> <sup>UDP</sup>	0.028	n.a.	n.a.	
SEM	0.003	n.a.	n.a.	

A sense construct containing the sequence of the coding region for cellulose synthase (CEL; SEQ ID NO: 50) from *Eucalyptus grandis* was inserted into the protein expression vector pcDNA3 (Invitrogen, Carlsbad, CA). The resulting construct was transfected into mammalian 293T cells (DuBridge RB et al., *Mol. Cell. Biol.* 7[1]:379-387, 1987), and recombinant protein was induced by the addition of IPTG. Proteins were solubilised from membranes, and the level of CEL activity was determined as described by Kudlicka K and Brown RM Jr. (*Plant Phys.* 115:643-656, 1997). As a positive control for activity, native CEL enzyme was solubilised from mung bean (*Vigna radiata*) plants. The determined levels of CEL activity for *V. radiata* are shown in Fig. 1. The levels of CEL activity found in mammalian 293T cells transfected with the *Eucalyptus* CEL expression clone were found to be similar to those obtained from *V. radiata* (Fig. 2). CEL activity was absent in nontransfected control 293T cells.

## Example 5

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## Use of a Cellulose Synthase (CEL) Gene to Modify Polysaccharide Biosynthesis

Transformation of tobacco plants with a *Pinus radiata* CEL gene is performed as follows. Genetic constructs comprising sense and anti-sense constructs containing a polynucleotide including the coding region of CEL (SEQ ID NO: 8) from *Pinus radiata* are constructed and inserted into *Agrobacterium tumefaciens* by direct transformation using published methods (*See*, An G, Ebert PR, Mitra A, Ha SB, "Binary Vectors," *in* Gelvin SB and Schilperoort RA, eds., *Plant Molecular Biology Manual*, Kluwer Academic Publishers: Dordrecht, 1988). The constructs of sense polynucleotides are made by cloning PBK-CMV plasmid cDNA inserts into pART7 plasmids, followed by cloning of the *Not*I-digested 35S-Insert-OCS 3'UTR-fragments from the pART7 vectors into pART27 plant expression vectors (*See* Gleave A, "A versatile binary vector system with a T-DNA organizational structure conducive to efficient integration of cloned DNA into the plant genome," *Plant Molecular Biology* 20:1203-1207, 1992). The presence and integrity of the transgenic constructs are verified by restriction digestion and DNA sequencing.

Tobacco (Nicotiana tabacum cv. Samsun) leaf sections are transformed with the sense and anti-sense CEL constructs using the method of Horsch et al. (Science 227:1229-1231,

1985). Transformed plants containing the appropriate CEL construct are verified using Southern blot experiments. Expression of *Pinus* CEL in transformed plants is confirmed by isolating total RNA from each independent transformed plant line created with the CEL sense and anti-sense constructs. The RNA samples are analysed in Northern blot experiments to determine the level of expression of the transgene in each transformed line.

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The total activity of CEL enzyme, encoded by the *Pinus* CEL gene and by the endogenous tobacco CEL gene, is analysed for each transformed plant line created with the CEL sense and anti-sense constructs. Crude protein extracts are prepared from each transformed plant and assayed using the methods of Robertson et al. (*Biochem J.* 306:745-750, 1995) and Pear et al. (*Proc. Natl. Acad. Sci. USA* 93:12637-12642, 1996).

The concentration of cellulose in the transformed tobacco plants is determined using the method of Smith and Harris (*Plant Phys.* 107:1399-1409, 1995). Briefly, whole tobacco plants, of an average age of 38 days, are frozen in liquid nitrogen and ground to a fine powder in a mortar and pestle. The cellulose content of 100 mg of frozen powder from an empty vector-transformed control plant line, at least one independent transformed plant line containing the sense construct for CEL and at least one independent transformed plant lines containing the anti-sense construct for CEL are determined using a glucan estimation kit from Megazyme (Warriewood, New South Wales, Australia) using the protocols supplied by the manufacturer.

SEQ ID NOS: 1-908 are set out in the attached Sequence Listing. The codes for nucleotide and amino acid sequences used in the attached Sequence Listing, including the symbols "n" and "Xaa", conform to WIPO Standard ST.25 (1998), Appendix 2, Table 1.

Although the present invention has been described in some detail by way of illustration and example for purposes of clarity of understanding, changes and modifications can be carried out without departing from the scope of the invention which is intended to be limited only by the scope of the claims.

## Claims:

- 1. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of: (1) sequences recited in SEQ ID NOS: 1-29, 57-80, 105, 107, 109-113, 119-129, 139-143 and 149-908; (2) complements of the sequences recited in SEQ ID NOS: 1-29, 57-80, 105, 107, 109-113, 119-129, 139-143 and 149-908; (3) reverse 5 complements of the sequences recited in SEQ ID NOS: 1-29, 57-80, 105, 107, 109-113, 119-129, 139-143 and 149-908; (4) reverse sequences of the sequences recited in SEQ ID NOS: 1-29, 57-80, 105, 107, 109-113, 119-129, 139-143 and 149-908; (5) nucleotide sequences producing an Expectation ("E") value of 0.01 or less when compared to a sequence recited in (1) - (4) above; (6) nucleotide sequences having at 10 least 50% identity to a nucleotide sequence recited in (1) - (4) above; (7) nucleotide sequences that hybridize to a sequence recited in (1) – (4) above under stringent hybridization conditions; (8) nucleotide sequences that are 200-mers of a sequence recited in (1) - (4) above; (9) nucleotide sequences that are 100-mers of a sequence recited in (1) - (4) above; (10) nucleotide sequences that are 40-mers of a sequence 15 recited in (1) - (4) above; (11) nucleotide sequences that are 20-mers of a sequence recited in (1) - (4) above; (12) nucleotide sequences that are degeneratively equivalent to a sequence recited in (1) - (4) above; and (13) nucleotide sequences that are allelic variants of a sequence recited in (1) - (4) above.
- 20 2. An isolated oligonucleotide probe or primer comprising at least 10 contiguous residues complementary to 10 contiguous residues of a nucleotide sequence recited in claim 1.
  - 3. A kit comprising a plurality of oligonucleotide probes or primers of claim 2.
  - 4. A storage medium having recorded thereon a plurality of polynucleotides, at least one of the polynucleotides comprising a nucleotide sequence recited in claims 1 or 2.
- 25 5. A construct comprising a polynucleotide of claim 1.
  - 6. A transgenic cell comprising a construct according to claim 5.
  - 7. A construct comprising, in the 5'-3' direction:
    - (a) a gene promoter sequence;

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(b) a polynucleotide sequence comprising at least one of the following: (1) a polynucleotide coding for at least a functional portion of a polypeptide

encoded by a nucleotide sequence of claim 1; and (2) a polynucleotide comprising a non-coding region of a gene coding for a polypeptide encoded by a nucleotide sequence selected from the group consisting of sequences recited in claim 1; and

5 (c) a gene termination sequence.

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- 8. The construct of claim 7, wherein the polynucleotide is in a sense orientation.
- 9. The construct of claim 7, wherein the polynucleotide is in an antisense orientation.
- 10. The construct of claim 7, wherein the gene promoter sequence is functional in a plant host to provide for transcription in xylem.
- 10 11. A transgenic plant cell comprising a construct of claim 7.
  - 12. A plant comprising a transgenic plant cell according to claim 11, or a part or propagule or progeny thereof.
  - 13. A method for modulating one or more of the polysaccharide content, the polysaccharide composition and the polysaccharide structure of a plant, comprising stably incorporating into the genome of the plant a polynucleotide of claim 1.
  - 14. The method of claim 13 wherein the plant is selected from the group consisting of eucalyptus and pine species.
  - 15. The method of claim 13 comprising stably incorporating into the genome of the plant a construct of claim 7.
- 20 16. A method for producing a plant having one or more of altered polysaccharide content, altered polysaccharide composition and altered polysaccharide structure, comprising:
  - (a) transforming a plant cell with a construct of claim 7 to provide a transgenic cell; and
  - (b) cultivating the transgenic cell under conditions conducive to regeneration and mature plant growth.
  - 17. A method for modifying the activity of a polypeptide involved in a polysaccharide biosynthetic pathway in a plant comprising stably incorporating into the genome of the plant a construct of claim 7.
- An isolated polypeptide comprising an amino acid sequence selected from the group consisting of: (a) sequences of SEQ ID NOS: 30-56, 81-104, 106, 108, 114-118, 129-138 and 144-148; (b) sequences having at least 50% identity to a sequence of (a);

sequences having at least 70% identity to a sequence of (a); and sequences having at least 90% identity to a sequence of (a).

19. An isolated polypeptide encoded by an isolated polynucleotide sequence of claim 1.

1/1 Figure 1

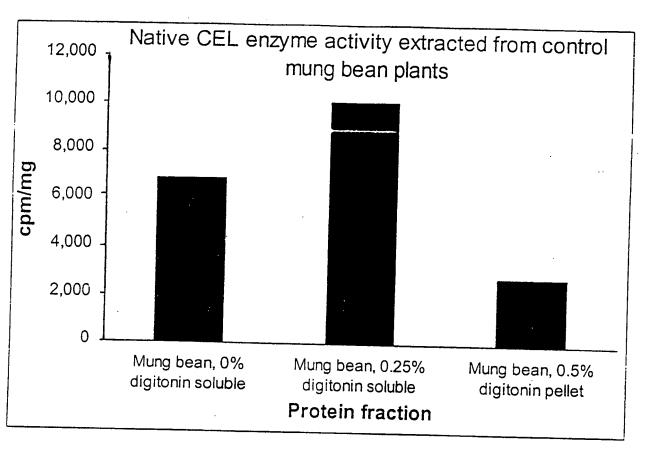
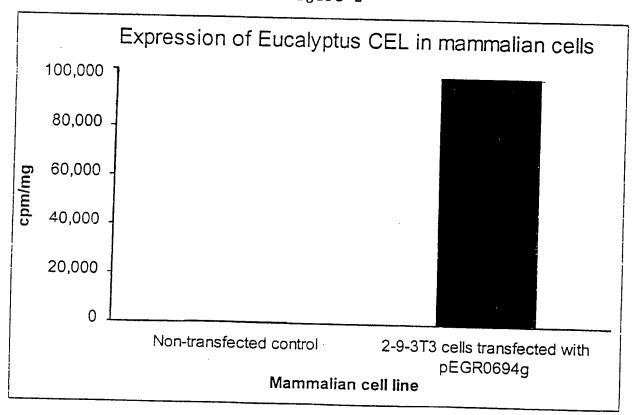


Figure 2



## SEQUENCE LISTING

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1620

1680

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Ser Ser Leu Cys Asp Tyr Arg Ile Phe Ala Asp Ser Lys Arg Lys
His Ala Ile Phe Arg Lys Gln Asn Ile Asn Arg Ser Thr Val Val Ser
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Pro Arg Ala Val Ser Asp Thr Phe Ser Glu Leu Thr Cys Leu Asp Pro
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Thr Arg Leu Tyr Pro Leu Thr Lys Lys Arg Ala Lys Pro Ala Val Pro
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Ser Glu Ile Ala Ser Leu Leu Ala Glu Gly Lys Val Pro Ile Gly Ile
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Gly Lys Asn Thr Lys Ile Arg Asn Cys Ile Ile Asp Lys Asn Ala Lys
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Ile Gly Lys Asp Val Ala Ile Val Asn Lys Asp Gly Val Glu Glu Ala
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Asp Arg Pro Gly Asp Gly Phe Tyr Ile Arg Leu Gly Ile Thr Val Ile
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Val Ala Leu His Asn Gln Tyr Trp Arg Leu Ile Asp Pro Gln Gly Lys
Pro Thr Gly Val Met Gly Trp Trp Pro Ser Arg Ala Val Thr Tyr Leu
Glu Asn His Asp Thr Gly Ser Thr Gln Gly His Trp Pro Phe Pro Arg
Asp Lys Leu Thr Gln Gly Tyr Ala Tyr Ile Leu Thr His Pro Gly Thr
Pro Thr Ile Phe Tyr Asp His Phe Tyr Asp Phe Gly Leu His Asp Thr
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                                105
Ile Thr Glu Leu Ile Asp Ala Arg Thr Arg Ala Gly Ile His Cys Arg
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Phe Gly Gly Arg Leu Asn Trp Asp Asp Arg Ala Val Val Ala Asp Asp
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145
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Gly Ser Thr Gln Gly His Trp Arg Phe Pro Ser Gly Lys Glu Met Gln
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Gly Tyr Ala Tyr Ile Leu Thr His Pro Gly Thr Pro Ala Val Phe Tyr
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Asp His Ile Phe Ser His Tyr Gln Ser Glu Ile Gly Ser Leu Ile Ser
Ile Arg Asn Arg Asn Lys Ile His Cys Arg Ser Thr Ile Lys Ile Thr
                        295
Lys Ala Glu Arg Asp Val Tyr Ala Ala Ile Ile Asp Asp Lys Val Ala
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                                        315
Met Lys Ile Gly Pro Gly Tyr Tyr Glu Pro Gln Ser
      <210> 36
      <211> 251
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      <213> Eucalyptus grandis
      <400> 36
Met Met Glu Ser Gly Val Pro Leu Cys Asn Thr Cys Gly Glu Ala Val
Gly Val Asp Glu Lys Gly Glu Val Phe Val Ala Cys Gln Glu Cys Asn
Phe Ala Ile Cys Lys Ala Cys Val Glu Tyr Glu Ile Lys Glu Gly Arg
                            40
Lys Ala Cys Leu Arg Cys Gly Thr Pro Phe Glu Ala Asn Ser Met Ala
Asp Ala Glu Arg Asn Glu Leu Gly Ser Arg Ser Thr Met Ala Ala Gln
Leu Asn Asp Pro Gln Asp Thr Gly Ile His Ala Arg His Ile Ser Ser
                                    90
Val Ser Thr Leu Asp Ser Glu Tyr Asn Asp Glu Thr Gly Asn Pro Ile
                                105
Trp Lys Asn Arg Val Glu Ser Trp Lys Asp Lys Lys Asn Lys Lys
                            120
Lys Ala Pro Thr Lys Ala Glu Lys Glu Ala Gln Val Pro Pro Glu Gln
                        135
                                            140
Gln Met Glu Glu Lys Gln Ile Ala Asp Ala Ser Glu Pro Leu Ser Thr
                   150
Val Ile Pro Ile Ala Lys Ser Lys Leu Ala Pro Tyr Arg Thr Val Ile
                                    170
Ile Met Arg Leu Ile Ile Leu Ala Leu Phe Phe His Tyr Arg Val Thr
                                185
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His Pro Val Asp Ser Ala Tyr Pro Leu Trp Leu Thr Ser Ile Ile Cys 195 200 205 Glu Ile Trp Phe Ala Tyr Ser Trp Val Leu Asp Gln Phe Pro Lys Trp

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210
                     215
Ser Pro Val Asn Arg Ile Thr His Val Asp Arg Leu Ser Ala Arg Tyr
                   230
                                 235
Glu Lys Glu Gly Glu Pro Ser Glu Leu Ala Val
               245
      <210> 37
      <211> 127
      <212> PRT
      <213> Pinus radiata
      <400> 37
Leu Pro Arg Leu Val Tyr Val Ser Arg Glu Lys Arg Pro Gly Tyr Gln
                                    10
His His Lys Lys Ala Gly Ala Met Asn Ala Leu Val Arg Val Ser Ala
                                25
Val Leu Thr Asn Ala Pro Phe Ile Leu Asn Leu Asp Cys Asp His Tyr
                            40
Leu Asn Asn Ser Lys Ala Val Arg Glu Ala Met Cys Phe Leu Met Asp
Pro Gln Leu Gly Lys Lys Leu Cys Tyr Val Gln Phe Pro Gln Arg Phe
                                        75
Asp Gly Ile Asp Arg His Asp Arg Tyr Ala Asn Arg Asn Thr Val Phe
                                    90
Phe Asp Ile Asn Met Lys Gly Leu Asp Gly Ile Gln Gly Pro Val Tyr
            100
                                105
Val Gly Thr Gly Cys Val Phe Asn Arg Gln Ala Leu Tyr Gly Tyr
                            120
      <210> 38
      <211> 534
      <212> PRT
      <213> Eucalyptus grandis
      <400> 38
His Tyr Ile Asn Asn Ser Lys Ala Ile Arg Glu Ala Met Cys Phe Leu
Met Asp Pro Gln Leu Gly Lys Lys Leu Cys Tyr Val Gln Phe Pro Gln
                                25
Arg Phe Asp Gly Ile Asp Arg His Asp Arg Tyr Ala Asn Arg Asn Ile
Val Phe Phe Asp Ile Asn Met Arg Gly Leu Asp Gly Ile Gln Gly Pro
Val Tyr Val Gly Thr Gly Cys Val Phe Asn Arg Gln Ala Leu Tyr Gly
Tyr Asp Pro Pro Val Ser Gln Lys Arg Pro Lys Met Thr Cys Asp Cys
                                    90
Trp Pro Ser Trp Cys Ser Cys Cys Cys Gly Gly Ser Arg Lys Ser Lys
                                105
Ser Lys Lys Asp Asp Thr Ser Leu Leu Gly Pro Val His Ala Lys
                            120
Lys Lys Lys Met Thr Gly Lys Asn Tyr Leu Lys Lys Lys Gly Ser Gly
                       135
Pro Val Phe Asp Leu Glu Asp Ile Glu Glu Gly Leu Glu Gly Phe Asp
                   150
                                       155
Glu Leu Glu Lys Ser Ser Leu Met Ser Gln Lys Asn Phe Glu Lys Arg
                165
                                    170
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Phe Gly Gln Ser Pro Val Phe Ile Ala Ser Thr Leu Met Glu Asp Gly
                                185
Gly Leu Pro Glu Gly Thr Asn Ser Thr Ser Leu Ile Lys Glu Ala Ile
                            200
His Val Ile Ser Cys Gly Tyr Glu Glu Lys Thr Glu Trp Gly Lys Glu
                        215
Ile Gly Trp Ile Tyr Gly Ser Val Thr Glu Asp Ile Leu Thr Gly Phe
                    230
                                        235
Lys Met His Cys Arg Gly Trp Lys Ser Val Tyr Cys Met Pro Lys Arg
                                    250
Pro Ala Phe Lys Gly Ser Ala Pro Ile Asn Leu Ser Asp Arg Leu His
            260
                                265
Gln Val Leu Arg Trp Ala Leu Gly Ser Val Glu Ile Phe Leu Ser Arg
                            280
His Cys Pro Leu Trp Tyr Ala Trp Gly Gly Lys Leu Lys Leu Glu
                        295
Arg Leu Ala Tyr Ile Asn Thr Ile Val Tyr Pro Phe Thr Ser Ile Pro
                                        315
Leu Leu Phe Tyr Cys Thr Ile Pro Ala Val Cys Leu Leu Thr Gly Lys
                325
                                    330
Phe Ile Ile Pro Thr Leu Thr Asn Phe Ala Ser Ile Trp Phe Leu Ala
                                345
                                                    350
Leu Phe Leu Ser Ile Ile Ala Thr Gly Val Leu Glu Leu Arg Trp Ser
                            360
Gly Val Ser Ile Glu Asp Trp Trp Arg Asn Glu Gln Phe Trp Val Ile
                       375
                                            380
Gly Gly Val Ser Ala His Leu Phe Ala Val Phe Gln Gly Leu Leu Lys
                    390
                                        395
Val Leu Ala Gly Val Asp Thr Asn Phe Thr Val Thr Ala Lys Ala Ala
                                    410
Glu Asp Ser Glu Phe Gly Glu Leu Tyr Leu Phe Lys Trp Thr Thr Leu
            420
                                425
Leu Ile Pro Pro Thr Thr Leu Ile Ile Leu Asn Met Val Gly Val Val
                            440
                                                445
Ala Gly Val Ser Asp Ala Ile Asn Asn Gly Tyr Gly Ser Trp Gly Pro
                        455
                                           460
Leu Phe Gly Lys Leu Phe Phe Ala Phe Trp Val Ile Val His Leu Tyr
                   470
                                        475
Pro Phe Leu Lys Gly Leu Met Gly Lys Gln Asn Arg Thr Pro Thr Ile
                                    490
Val Val Leu Trp Ser Val Leu Leu Ala Ser Ile Phe Ser Leu Val Trp
                                505
Val Arg Ile Asp Pro Phe Leu Pro Lys Gln Thr Gly Pro Val Leu Lys
                            520
Pro Cys Gly Val Glu Cys
   530
      <210> 39
      <211> 133
      <212> PRT
     <213> Pinus radiata
     <400> 39
Leu Ala Leu Phe Leu Thr Trp Arg Val Lys Asn Pro Asn Thr Asp Ala
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10

Tyr Trp Leu Trp Gly Met Ser Ile Val Cys Glu Leu Trp Phe Ala Phe

20

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Ser Trp Leu Leu Asp Gln Leu Pro Lys Leu Cys Pro Ile Asn Arg Ser
                             40
Thr Asp Leu Ala Val Leu Lys Asp Lys Phe Glu Ser Pro Thr Gly Asp
                        55
Asn Pro Ala Gly Arg Ser Asp Leu Pro Gly Ile Asp Cys Phe Val Ser
                    70
                                        75
Thr Ala Asp Pro Glu Lys Glu Pro Pro Leu Val Thr Ala Asn Thr Ile
Leu Ser Ile Leu Ser Ala Asp Tyr Pro Val Glu Lys Leu Ala Cys Tyr
                                105
Val Ser Asp Asp Gly Gly Ala Leu Leu Thr Phe Glu Ala Met Ala Glu
                            120
Ala Ala Ser Phe Ala
    130
      <210> 40
      <211> 206
      <212> PRT
      <213> Pinus radiata
      <400> 40
Leu Leu Val Ser Gln Arg Ser Phe Glu Lys Ser Phe Gly Gln Ser Ser
Val Phe Ile Ala Ser Thr Leu Met Asp Asn Gly Gly Val Pro Glu Ser
Thr Asn Pro Ala Ser Leu Ile Lys Glu Ala Ile His Val Ile Ser Cys
                            40
Gly Tyr Glu Glu Lys Thr Glu Trp Gly Lys Glu Val Gly Trp Ile Tyr
Gly Ser Val Thr Glu Asp Ile Leu Thr Gly Phe Lys Met His Cys Arg
Gly Trp Arg Ser Ile Tyr Cys Met Pro Lys Arg Pro Ala Phe Lys Gly
                                    90
Ser Ala Pro Ile Asn Leu Ser Asp Arg Leu His Gln Val Leu Arg Trp
                                105
Ala Leu Gly Ser Ile Glu Ile Leu Phe Ser Arg His Cys Pro Leu Trp
                            120
Tyr Gly Phe Gly Ala Gly Arg Leu Lys Trp Leu Glu Arg Leu Ala Tyr
                        135
Thr Asn Thr Ile Val Tyr Pro Leu Thr Ser Leu Pro Leu Ile Ala Tyr
                    150
                                        155
Cys Thr Leu Pro Ala Ile Cys Leu Leu Thr Gly Glu Phe Ile Ile Pro
                165
                                    170
Thr Leu Ser Asn Leu Ala Ser Ile Tyr Phe Met Leu Leu Phe Ile Ser
            180
                                185
Ile Ile Val Thr Gly Val Leu Glu Leu Arg Trp Ser Gly Val
                            200
      <210> 41
      <211> 239
      <212> PRT
      <213> Eucalyptus grandis
      <400> 41
Leu Ala Leu Arg His Asp Arg Glu Gly Glu Pro Ser Gln Leu Ala Pro
Val Asp Val Phe Val Ser Thr Val Asp Pro Leu Lys Glu Pro Pro Leu
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Ile Thr Ala Asn Thr Val Leu Ser Ile Leu Ala Val Asp Tyr Pro Val
                            40
Asp Lys Val Ser Cys Tyr Val Ser Asp Gly Ser Ala Met Leu Thr
                        55
Phe Glu Ala Leu Ser Glu Thr Ala Glu Phe Ala Arg Lys Trp Val Pro
Phe Cys Lys Lys His Asn Ile Glu Pro Arg Ala Pro Glu Phe Tyr Phe
                                    90
Ala Gln Lys Ile Asp Tyr Leu Lys Asp Lys Ile Gln Pro Ser Phe Val
                                105
Lys Glu Arg Arg Ala Met Lys Arg Glu Tyr Glu Glu Phe Lys Val Arg
                            120
Ile Asn Ala Leu Val Ala Lys Ala Gln Lys Met Pro Glu Glu Gly Trp
                        135
Thr Met Gln Asp Gly Thr Ala Trp Pro Gly Asn Asn Pro Arg Asp His
                    150
                                        155
Pro Gly Met Ile Gln Val Phe Leu Gly His Ser Gly Gly Leu Asp Thr
                                    170
Asp Gly Asn Glu Leu Pro Arg Leu Val Tyr Val Ser Arg Glu Lys Arg
                                185
Pro Gly Phe Gln His His Lys Lys Ala Gly Ala Met Asn Ala Leu Ile
                            200
Arg Val Ser Ala Val Leu Thr Asn Gly Ala Tyr Leu Leu Asn Val Asp
                        215
Cys Asp His Tyr Phe Asn Asn Ser Lys Ala Leu Lys Glu Ala Met
                    230
      <210> 42
      <211> 253
      <212> PRT
      <213> Eucalyptus grandis
      <400> 42
Ile Ser Cys Gly Tyr Glu Asp Lys Thr Glu Trp Gly Lys Glu Ile Gly
                                    10
Trp Ile Tyr Gly Ser Val Thr Glu Asp Ile Leu Thr Gly Phe Lys Met
                                25
His Ala Arg Gly Trp Ile Ser Ile Tyr Cys Met Pro Pro Arg Pro Ala
Phe Lys Gly Ser Ala Pro Ile Asn Leu Ser Asp Arg Leu Asn Gln Val
Leu Arg Trp Ala Leu Gly Ser Ile Glu Ile Leu Leu Ser Arg His Cys
                                        75
Pro Ile Trp Tyr Gly Tyr Asn Gly Lys Leu Arg Leu Leu Glu Arg Leu
                                    90
Ala Tyr Ile Asn Thr Ile Val Tyr Pro Leu Thr Ser Ile Pro Leu Ile
                                105
Ala Tyr Cys Ile Leu Pro Ala Phe Cys Leu Leu Thr Asn Lys Phe Ile
                            120
Ile Pro Glu Ile Ser Asn Phe Ala Ser Met Trp Phe Ile Leu Leu Phe
                        135
Val Ser Ile Phe Thr Thr Gly Ile Leu Glu Leu Arg Trp Ser Gly Val
                    150
Ser Ile Glu Asp Trp Trp Arg Asn Glu Gln Phe Trp Val Ile Gly Gly
                                    170
Thr Ser Ala His Leu Phe Ala Val Phe Gln Gly Leu Leu Lys Val Leu
```

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180
                               185
Ala Gly Ile Asp Thr Asn Phe Thr Val Thr Ser Lys Ala Gly Asp Glu
                           200
Asp Gly Asp Phe Ala Glu Leu Tyr Val Phe Lys Trp Thr Ser Leu Leu
            215
Ile Pro Pro Thr Thr Val Leu Ile Val Asn Ile Ile Gly Ile Val Ala
                    230
                                        235
Gly Val Ser Tyr Ala Ile Asn Ser Gly Tyr Gln Ser Trp
      <210> 43
      <211> 469
      <212> PRT
      <213> Eucalyptus grandis
      <400> 43
Gln Cys Phe Ser Ile Leu Ala Val Asp Tyr Pro Val Asp Lys Val Ser
Cys Tyr Leu Ser Asp Asp Gly Ala Ala Met Leu Ser Phe Glu Ser Leu
Val Glu Thr Ala Asp Phe Ala Arg Lys Trp Val Pro Phe Cys Lys Lys
Tyr Ser Ile Glu Pro Arg Ala Pro Glu Phe Tyr Phe Ser Gln Lys Ile
                        55
Asp Tyr Leu Lys Asp Lys Ile Gln Pro Ser Phe Val Lys Glu Arg Arg
                                        75
Ala Met Lys Arg Asp Tyr Glu Glu Phe Lys Val Arg Val Asn Ala Leu
                85
                                    90
Val Ala Lys Ala Gln Lys Ala Pro Glu Glu Gly Trp Ser Met Gln Asp
                                105
Gly Thr Pro Trp Pro Gly Asn Asn Ser Arg Asp His Pro Gly Met Ile
                            120
Gln Val Phe Leu Gly Ser Ser Gly Ala His Asp Ile Glu Gly Asn Glu
                        135
Leu Pro Arg Leu Val Tyr Val Ser Arg Glu Lys Arg Pro Gly Phe Gln
                    150
                                       155
His His Lys Lys Ala Gly Ala Glu Asn Ala Leu Val Arg Val Ser Ala
                                   170
Ile Leu Thr Asn Ala Pro Tyr Ile Leu Asn Leu Asp Cys Asp His Tyr
                               185
Val Asn Tyr Ser Asn Ala Val Arg Glu Ala Met Cys Phe Leu Met Asp
                            200
Pro Gln Val Gly Arg Asn Leu Cys Tyr Val Gln Phe Pro Gln Arg Phe
                        215
                                           220
Asp Gly Ile Asp Arg Ser Asp Arg Tyr Ala Asn Arg Asn Thr Val Phe
                    230
                                       235
Phe Asp Val Asn Met Lys Gly Leu Asp Gly Ile Gln Gly Pro Val Tyr
               245
                                   250
Val Gly Thr Gly Cys Val Phe Asn Arg Gln Ala Leu Tyr Gly Tyr Gly
            260
                               265
Pro Pro Ser Met Pro Asn Leu Pro Lys Pro Ser Ser Ser Cys Ser Trp
       275
                           280
Cys Gly Cys Cys Ser Cys Cys Cys Pro Ser Lys Lys Pro Thr Lys Asp
                        295
Leu Ser Glu Val Tyr Arg Asp Ser Lys Arg Glu Asp Leu Asn Ala Ala
                                       315
Ile Phe Asn Leu Gly Glu Ile Asp Asn Tyr Asp Glu His Glu Arg Ser
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330 325 Met Leu Ile Ser Gln Met Ser Phe Glu Lys Thr Phe Gly Leu Ser Thr 340 345 Val Phe Ile Glu Ser Thr Leu Leu Ala Asn Gly Gly Val Pro Glu Ser 360 Ala His Pro Ser Met Leu Ile Lys Glu Ala Ile His Val Ile Ser Cys 375 380 Gly Tyr Glu Glu Lys Thr Ala Trp Gly Lys Glu Ile Gly Trp Ile Tyr 390 395 Gly Ser Val Thr Glu Asp Ile Leu Thr Gly Phe Lys Met His Cys Arg 405 410 Gly Trp Arg Ser Val Tyr Cys Met Pro Leu Arg Pro Ala Phe Lys Gly 420 425 Ser Ala Pro Ile Asn Leu Ser Asp Arg Leu His Gln Val Leu Arg Trp 440 Ala Leu Gly Ser Val Glu Ile Phe Leu Ser Arg His Cys Pro Leu Trp 455 Tyr Gly Phe Gly Gly 465 <210> 44 <211> 805 <212> PRT <213> Eucalyptus grandis <400> 44 Met Ala Asp Arg Met Leu Thr Arg Ser His Ser Leu Arg Glu Arg Leu Asp Glu Thr Leu Ser Ala His Arg Asn Asp Ile Val Ala Phe Leu Ser 25 Arg Val Glu Ala Lys Gly Lys Gly Ile Leu Gln Arg His Gln Ile Phe 40 Ala Glu Phe Glu Ala Ile Ser Glu Glu Ser Arg Ala Lys Leu Leu Asp 55 Gly Ala Phe Gly Glu Val Leu Lys Ser Thr Gln Glu Ala Ile Val Ser Pro Pro Trp Val Ala Leu Ala Val Arg Pro Arg Pro Gly Val Trp Glu His Ile Arg Val Asn Val His Ala Leu Val Leu Glu Gln Leu Glu Val 105 Ala Glu Tyr Leu His Phe Lys Glu Glu Leu Ala Asp Gly Ser Leu Asn 120 125 Gly Asn Phe Val Leu Glu Leu Asp Phe Glu Pro Phe Thr Ala Ser Phe 135 140 Pro Arg Pro Thr Leu Ser Lys Ser Ile Gly Asn Gly Val Glu Phe Leu Asn Arg His Leu Ser Ala Lys Leu Phe His Asp Lys Glu Ser Leu His 165 170 Pro Leu Leu Glu Phe Leu Gln Val His Cys Tyr Lys Gly Lys Asn Met

235

220

180 185 190

Met Val Asn Ala Arg Ile Gln Asn Val Phe Ser Leu Gln His Val Leu
195 200 205

Arg Lys Ala Glu Glu Tyr Leu Thr Ser Leu Lys Pro Glu Thr Pro Tyr

Ser Gln Phe Glu His Lys Phe Gln Glu Ile Gly Leu Glu Arg Gly Trp

Gly Asp Thr Ala Glu Arg Val Leu Glu Met Ile Gln Leu Leu Asp

215

230

				245											
T 0	τ	<b>a</b> 1	7 T -	245		<b>.</b>	_	_,	250		_		_	255	
			260					265					270	_	Arg
Val	Pro	Met 275		Phe	Asn	Val	Val 280		Met	Ser	Pro	His 285	Gly	Tyr	Phe
Ala	Gln 290		Asp	Val	Leu	Gly 295		Pro	Asp	Thr	Gly 300	Gly	Gln	Val	Val
Tyr 305		Leu	Asp	Gln	Val 310	Arg	Ala	Leu	Glu	Glu 315		Met	Leu	His	Arg 320
Ile	Lys	Gln	Gln	Gly 325	Leu	Asp	Ile	Thr	Pro		Ile	Leu	Ile	Ile 335	Thr
Arg	Leu	Leu	Pro 340	Asp	Ala	Val	Gly	Thr	Thr	Cys	Gly	Gln	Arg 350		Glu
Lys	Val	Phe	Gly		Glu	Tyr	Ser 360			Leu	Arg	Val 365		Phe	Arg
Asn	Glu 370			Val	Val	Arg	Lys	Trp	Ile	Ser	Arg 380		Glu	Val	Trp
Pro 385		Leu	Glu	Arg	Tyr 390			Asp	Val	Ala 395		Glu	Leu	Ala	Gly 400
Glu	Leu	Gln	Gly	Lys 405	Pro	Asp	Leu	Ile	Ile 410		Asn	Tyr	Ser	Asp	Gly
Asn	Ile	Val	Ala 420	Ser	Leu	Leu	Ala	His 425		Leu	Gly	Val	Thr 430		Cys
Thr	Ile	Ala 435	His	Ala	Leu	Glu	Lys 440		Lys	Tyr	Pro	Glu 445		Asp	Ile
Tyr	Trp 450	Lys	Lys	Phe	Glu	Glu 455	Lys	Tyr	His	Phe	Ser 460		Gln	Phe	Thr
Ala 465	Asp	Leu	Ile	Ala	Met 470	Asn	His	Thr	Asp	Phe 475		Ile	Thr	Ser	Thr 480
Phe	Gln	Glu	Ile	Ala 485	Gly	Ser	Lys	Asp	Thr 490		Gly	Gln	Tyr	Glu 495	Ser
His	Met	Asn	Phe 500	Thr	Leu	Pro	Gly	Leu 505	Tyr	Arg	Val	Val	His 510	Gly	Ile
		515			Lys		520					525	Ala		
	530				Tyr	535					540		•		
545					Glu 550					555				_	560
				565	Lys				570					575	
			580		Val			585					590		
		595			Leu		600					605			_
	610				Asp	615					620				
625					Leu 630					635					640
				645	Gln				650					655	_
			660		Thr			665					670		
		675			Thr		680					685			
Thr	Phe 690	Ala	Thr	Cys	Asn	Gly 695	Gly	Pro	Ala	Glu	11e 700	Ile	Val	His	Gly

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Lys Ser Gly Tyr His Ile Asp Pro Tyr His Gly Asp Gln Ala Ala Glu
                     710
                                         715
Leu Leu Val Asp Phe Phe Asn Lys Cys Lys Ile Asp Gln Ser His Trp
                 725
                                    730
Asp Glu Ile Ser Lys Gly Ala Met Gln Arg Ile Glu Glu Lys Tyr Thr
                                745
Trp Lys Ile Tyr Ser Glu Arg Leu Leu Asn Leu Thr Ala Val Tyr Gly
                             760
Phe Trp Lys His Val Thr Asn Leu Asp Arg Arg Glu Ser Arg Arg Tyr
                         775
Leu Glu Met Phe Tyr Ala Leu Lys Tyr Arg Pro Leu Ala Gln Ser Val
                    790
                                         795
Pro Pro Ala Val Glu
      <210> 45
      <211> 133
      <212> PRT
      <213> Pinus radiata
      <400> 45
Ile Lys Gln Gln Gly Leu Asp Ile Thr Pro Gln Ile Ile Val Val Thr
                                     10
Arg Leu Ile Pro Glu Ala His Gly Thr Thr Cys Asn Gln Arg Ile Glu
                                 25
Lys Val Ser Gly Thr Gln His Ser Leu Ile Leu Arg Val Pro Phe Arg
                            40
Thr Glu Lys Gly Val Leu Arg Asn Trp Val Ser Arg Phe Asp Val Trp
Pro Tyr Leu Glu Arg Phe Ser Glu Asp Val Thr Asn Glu Val Thr Ala
                                        75
Glu Leu Lys Gly Gln Pro Asp Leu Ile Ile Gly Asn Tyr Ser Asp Gly
                                    90
Asn Leu Val Ala Ser Leu Ile Ala His Lys Gln Gly Ile Thr Gln Cys
                                105
Asn Ile Ala His Ala Leu Glu Lys Thr Lys Tyr Pro Asp Ser Asp Ile
        115
                            120
Tyr Trp Lys Asn Phe
    130
      <210> 46
      <211> 158
      <212> PRT
      <213> Pinus radiata
      <400> 46
His Gly Ile Asp Val Phe Asp Pro Lys Phe Asn Ile Val Ser Pro Gly
Ala Asp Met Gln Ile Tyr Phe Pro Tyr Thr Glu Lys Gln His Arg Leu
                                25
Thr Thr Leu His Gly Thr Ile Glu Glu Leu Leu Phe Ser Pro Glu Gln
                            40
Thr Ala Glu His Met Cys Ala Leu Asn Asp Arg Lys Lys Pro Ile Ile
Phe Ser Met Ala Arg Leu Asp Arg Val Lys Asn Met Thr Gly Leu Val
Glu Trp Phe Ala Lys Ser Lys Arg Leu Arg Glu Leu Val Asn Leu Val
```

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85
                                    90
Val Val Ala Gly Asp Ile Asp Pro Ser Lys Ser Lys Asp Arg Glu Glu
            100
                               105
Val Ala Glu Ile Glu Lys Met His Arg Leu Val Lys Glu Tyr Asn Leu
                            120
Asn Gly Gln Phe Arg Trp Ile Cys Ala Gln Lys Asn Arg Val Arg Asn
                        135
Gly Glu Leu Tyr Arg Tyr Ile Cys Asp Thr Arg Gly Ala Phe
                    150
      <210> 47
      <211> 144
      <212> PRT
      <213> Eucalyptus grandis
      <400> 47
Met Ala Asp Arg Val Leu Asn Arg Ser His Ser Pro Arg Glu Arg Leu
Asp Glu Ala Leu Phe Ala Asp Arg Asn Asp Cys Leu Val Phe Leu Ser
                                25
Arg Leu Lys Ala Lys Gly Lys Gly Ile Leu Gln Arg His Gln Ile Leu
                            40
Ala Val Phe Glu Ala Ile Pro Glu Glu Ser Arg Ala Arg Leu Leu Asp
                        55
Gly Ala Phe Gly Lys Val Leu Lys Ser Thr Gln Glu Ala Ile Val Ser
                    70
Ser Pro Trp Val Ala Leu Ala Val Arg Ala Arg Pro Gly Val Trp Glu
                                    90
His Ile Arg Val Asn Val His Ala Leu Leu Leu Glu His Phe Gln Val
                                105
Asp Glu Tyr Leu His Phe Lys Glu Ala Leu Val Asp Gly Ser Leu Asn
                            120
Pro Asp Ser Glu Pro Leu Thr Ala Thr Phe Gly Arg Arg Pro Phe His
                        135
      <210> 48
      <211> 90
      <212> PRT
      <213> Eucalyptus grandis
      <400> 48
Gln Glu Ala Ile Val Ser Pro Pro Trp Val Ala Leu Ala Val Arg Pro
                                    10
Arg Pro Gly Val Trp Glu His Ile Arg Val Asn Val His Ala Leu Val
Leu Glu Gln Leu Glu Val Ala Glu Tyr Leu His Phe Lys Glu Glu Leu
                            40
Ala Asp Gly Ser Leu Asn Gly Asn Phe Val Leu Glu Leu Asp Phe Glu
                        55
                                            60
Pro Phe Thr Ala Ser Phe Pro Arg Pro Thr Leu Ser Lys Ser Ile Gly
                    70
Asn Gly Val Glu Phe Arg Asn Arg His Leu
      <210> 49
      <211> 247
      <212> PRT
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## <213> Pinus radiata

<400> 49 Met Ala Ala Pro Ala Val Ala Ser Pro Ala Ala Glu Thr Asp Arg Ile Pro Lys Leu Gln Ala Glu Val Thr Lys Leu Asn Gln Ile Ser Asp Asn Glu Lys Glu Gly Phe Val Arg Leu Val Ser Arg Tyr Leu Ser Gly 40 Glu Glu Glu Lys Ile Glu Trp Glu Lys Ile Lys Thr Pro Thr Asp Glu Ile Val Val Pro Tyr Asp Thr Leu Ala Ala Leu Gly Glu Asp Pro Ser 75 Glu Thr Lys Glu Leu Leu Asp Lys Leu Val Val Leu Lys Leu Asn Gly 85 Gly Leu Gly Thr Thr Met Gly Cys Thr Gly Pro Lys Ser Val Ile Glu 105 Val Arg Asn Gly Leu Thr Phe Leu Asp Leu Ile Val Lys Gln Ile Glu 120 Ser Leu Asn Asn Lys Tyr Asp Ser Lys Val Pro Leu Val Leu Met Asn 135 Ser Phe Asn Thr His Asp Asp Thr Ile Lys Ile Val Glu Lys Tyr Ser 150 Gly Ser Asn Ile Asp Ile His Ile Phe Asn Gln Ser Gln Tyr Pro Arg 165 170 Met Val Ala Glu Asp Leu Thr Pro Trp Pro Thr Lys Gly Arg Thr Asp 180 185 Lys Glu Ala Trp Tyr Pro Pro Gly His Gly Asp Val Phe Pro Ala Leu 200 Leu Asn Ser Gly Lys Leu Asp Glu Leu Leu Ser Gln Gly Lys Glu Tyr 215 220 Val Phe Ile Ala Asn Ser Asp Asn Leu Gly Ala Ile Val Asp Leu Ser 235 Ile Leu Phe Ala Leu Val Phe 245

<210> 50

<211> 103

<212> PRT

<213> Eucalyptus grandis

<400> 50

 Met
 Ala
 Ala
 Ala
 Ala
 Ala
 Thr
 Leu
 Ser
 Ala
 Pro
 Asp
 Ala
 Ala
 Lys
 Leu
 Ser
 Ala
 Pro
 Asp
 Ala
 Ala
 Lys
 Leu
 Ser
 Ala
 A

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<210> 51
       <211> 253
       <212> PRT
       <213> Pinus radiata
      <400> 51
Ala Asn Ser Asp Asn Leu Gly Ala Ile Val Asp Leu Lys Ile Leu Asn
His Leu Val Lys Asn Lys Asn Glu Tyr Cys Met Glu Val Thr Pro Lys
Thr Leu Ala Asp Val Lys Gly Gly Thr Leu Ile Ser Tyr Glu Gly Arg
Val Gln Leu Leu Glu Ile Ala Gln Val Pro Glu Glu His Val Gly Glu
                        55
Phe Lys Ser Ile Glu Lys Phe Lys Ile Phe Asn Thr Asn Asn Leu Trp
                    70
Val Asn Leu Lys Ala Ile Lys Arg Leu Val Glu Ala Asp Ala Leu Lys
Met Glu Ile Ile Pro Asn Pro Lys Glu Val Asp Gly Val Lys Val Leu
                                105
Gln Leu Glu Thr Ala Ala Gly Ala Ala Ile Arg Phe Phe Asp Arg Ala
                            120
Ile Gly Val Asn Val Pro Arg Ser Arg Phe Leu Pro Val Lys Ala Thr
                        135
                                            140
Ser Asp Leu Leu Val Gln Ser Asp Leu Tyr Thr Val Glu Gly
                   150
                                        155
Phe Val Ile Arg Asn Pro Ala Arg Val Asn Pro Thr Asn Pro Thr Ile
                                    170
Glu Leu Gly Pro Glu Phe Lys Lys Val Gly Asn Phe Leu Lys Arg Phe
Lys Ser Ile Pro Ser Ile Ile Asp Leu Asp Ser Leu Lys Val Ser Gly
                            200
Asp Val Trp Phe Gly Ser Gly Val Ile Leu Lys Gly Lys Val Ile Ile
                        215
                                            220
Glu Ala Lys Gln Gly Ala Thr Leu Glu Ile Pro Asp Glu Ser Val Ile
                    230
                                        235
Glu Asn Lys Val Val Ser Ser Pro Asp Asp Ile Val Asn
                245
                                    250
      <210> 52
      <211> 184
      <212> PRT
      <213> Pinus radiata
      <400> 52
Met Ser Thr Ile Ile Val Pro Val Pro Ile Pro Thr Pro Ser Glu Asp
Ser Glu Arg Leu Arg Lys Ala Phe Glu Gly Trp Gly Thr Asn Glu Lys
                                25
Ser Ile Ile Gln Ile Leu Gly His Arg Thr Ala Ala Gln Arg Lys Val
                            40
Ile Arg Gln Ser Tyr Phe Gln Leu Tyr Glu Glu Asp Leu Leu Lys Arg
Leu Glu Ser Glu Leu Ser Ser Asp Phe Glu Lys Ala Val Phe Leu Trp
                                        75
Val Leu Asp Pro Ala Glu Arg Asp Ala Val Ile Ser His Gly Ala Ile
```

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Lys Lys Trp Asn Ala Lys Asn Ile Ser Leu Leu Glu Ile Ser Ser Ala
                                 105
Arg Ser Ser Ala Glu Leu Leu Met Val Arg Gln Ala Tyr His Ile Arg
                            120
                                                 125
Asp Lys Lys Ser Leu Glu Glu Asp Val Ala Ala His Thr Ser Gly Asn
                        135
Phe Arg Lys Leu Leu Val Ala Leu Val Ser Ser Tyr Arg Tyr Glu Gly
                    150
                                        155
Pro Glu Val Asp Met His Leu Ala Ser Tyr Glu Ala Lys Lys Leu Ser
                                     170
Glu Ser Ile Thr Glu Gln Lys Arg
            180
      <210> 53
      <211> 213
      <212> PRT
      <213> Pinus radiata
      <400> 53
Met Ala Thr Cys Ser Cys Ala Val Ser Cys Gly Val Asn Pro Val Glu
Arg Asp Cys Glu Glu Ile His Leu Ala Cys Lys Gly Leu Gly Ser Asp
Glu Glu Lys Ile Ile Glu Ile Leu Gly Ser Lys Asn Glu Gln Gln Arg
Lys Glu Ile Arg Glu Thr Tyr Tyr Ala Met Tyr Lys Glu Asp Leu Cys
Lys Arg Leu Glu Lys Glu Leu His Gly Lys Leu Glu Lys Ala Ile Val
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Leu Trp Met His Glu Pro Ala Asp Arg Asp Ala Ile Ile Ala Gly Thr
Ala Leu Glu Gly Trp Cys Thr Asp Asp Arg Ala Leu Ile Glu Val Ile
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Cys Thr Arg Ser Ser Thr Gln Ile Val Lys Ile Arg Glu Ala Tyr Gln
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Lys Arg Tyr Gln Arg Cys Leu Asp Asp Val Ile Cys Lys Thr Asn
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Glu Cys Lys Gly Val Asp Ile Asn Lys Ala Arg Cys Asp Ala Lys Met
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attgaaaagt tcaaaatctt caataccaat aatttatggg tgaacttgaa ggcgattaag
                                                                    1260
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gcaattggtg tcaatgttcc aagatcacgc tttctcccag tgaaggcaac ttcagattta
                                                                    1440
ctacttgtgc agtcggatct ttacactgtg gaggaaggtt ttgtcatccg aaatcctgct
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agagtcaacc ctacaaatcc caccattgag ttgggtcctg aattcaagaa ggttggcaac
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tttctaaagc gtttcaagtc catacctagc atcattgatc ttgatagtct aaaggtgtca
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ggtgatgtgt ggtttggcag tggagtcatc ctgaagggaa aagttataat tgaagcaaag
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cagggggcta cacttgagat acctgatgaa tctgtgatag aaaacaaggt agtgagcagt
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cctgatgata ttgtgaacta gcttataagt tttggcagtt ggcattcttg atttttgggt
                                                                    1800
tgtttgtaga gctagaatac tgtgtttagt gcccttaaag agtagggtgg aagtttcacc
                                                                    1860
tetggtttta tettecataa teettaetgg gaggggttte ataattttat tataactage
                                                                    1920
cagtttctat gtaaatgttg agcgcgaatt tttatgcatg aaagcctagg atgaagcatc
                                                                    1980
2040
aaaaa
                                                                    2045
     <210> 81
     <211> 139
     <212> PRT
     <213> Eucalyptus grandis
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<400> 81

Phe Asp Phe Ala Arg Gly Tyr Ser Pro Lys Tyr Val Lys Glu Tyr Ile Glu Ser Ala Lys Pro Leu Phe Ser Val Gly Glu Tyr Trp Asp Ser Cys Asn Tyr Ser Gly Thr Thr Leu Glu Tyr Asn Gln Asp Ser His Arg Gln Arg Ile Val Asn Trp Ile Asp Gly Thr Gly Gln Leu Ser Ala Ala Phe Asp Phe Thr Thr Lys Gly Ile Leu Gln Glu Ala Val Lys Gly Gln Phe Trp Arg Leu Arg Asp Pro Lys Gly Lys Pro Pro Gly Val Met Gly Trp 90 Trp Pro Ser Arg Ala Val Thr Phe Leu Asp Asn His Asp Thr Gly Ser 105 Thr Gln Ala His Trp Pro Phe Pro Ser Asn His Ile Arg Arg Val Thr 120 Arg Thr Tyr Ser Leu Ile Gln Glu Tyr Leu Leu 135

<210> 82

<211> 189

<212> PRT

<213> Eucalyptus grandis

<400> 82

Leu Phe Trp Leu Phe Val Leu Leu Val Phe Tyr Leu Ala Ala Ser Ala Ser Pro Ala Leu Leu Phe Gln Gly Phe Asn Trp Glu Ser Trp Lys Lys Glu Gly Gly Trp Tyr Asn Ser Leu Lys Asn Leu Val Pro Asp Leu Ala Asn Ala Gly Ile Thr His Val Trp Leu Pro Pro Pro Ser Gln Ser Ala 55 Ala Gln Gln Gly Tyr Leu Pro Gly Arg Leu Tyr Asp Leu Asn Ala Ser Ser Tyr Gly Asn Gln Asp Glu Leu Lys His Leu Ile Asp Ala Phe His 85 90 Gln Lys Gly Ile Lys Cys Leu Ala Asp Ile Val Ile Asn His Arg Thr 105 Ala Glu Lys Gln Asp Ser Arg Gly Ile Trp Cys Ile Phe Glu Gly Gly 120 Thr Pro Asp Asp Arg Leu Asp Trp Gly Pro Ser Leu Ile Cys Arg Asp 135 Asp Thr Glu Tyr Ser Asp Gly Arg Gly Asn Leu Asp Ser Gly Glu Asp 155 Phe Lys Pro Ala Pro Asp Ile Asp His Leu Asn Pro Arg Val Gln Lys 165 170 Glu Leu Ser Asp Trp Met Asn Trp Leu Lys Ser Asp Ile 180

185

<210> 83

<211> 176

<212> PRT

<213> Eucalyptus grandis

<400> 83 Phe Gly Glu Phe Asn Thr Asp Glu Met Ala Gly Val Met Ala Ala Gly 10 Val Ala Asn Leu Asn Val Leu Gly Arg Glu Thr Ala Glu Phe Thr Ser 20 Phe Arg Pro Val Phe Leu Arg Gly Asn Ser Gln Gly Leu Ser Ser Ala Ser Ser Leu Cys Asp Tyr Arg Ile Phe Ala Asp Ser Lys Arg Lys Lys 55 His Ala Ile Phe Arg Lys Gln Asn Ile Asn Arg Ser Thr Val Val Ser Pro Arg Ala Val Ser Asp Thr Phe Ser Glu Leu Thr Cys Leu Asp Pro 85 90 Val Ala Ser Arg Ser Val Leu Gly Ile Ile Leu Gly Gly Gly Ala Gly 100 105 Thr Arg Leu Tyr Pro Leu Thr Lys Lys Arg Ala Lys Pro Ala Val Pro 120 Leu Gly Ala Asn Tyr Arg Leu Ile Asp Ile Pro Val Ser Asn Cys Ile Asn Ser Asn Ile Ser Lys Ile Tyr Val Leu Thr Gln Phe Asn Ser Ala 150 155 Ser Leu Asn Pro Ser Ser Phe Thr Gly Leu Phe Lys His Met Gly Ser 170 <210> 84 <211> 47 <212> PRT <213> Eucalyptus grandis <400> 84 Asp Pro Ala Leu Asp Ser Ala Asp Ala Phe Lys Ser Val Arg Arg Asp Pro Asp Val Val Ser Pro Arg Asp Val Ser Asp Ser Arg Asn Ser Gln Thr Cys Leu Asn Pro Asp Ala Ser Arg Ser Val Leu Gly Ile Ile <210> 85 <211> 146 <212> PRT <213> Eucalyptus grandis <400> 85 Ala Pro Ala Leu Ala Ser Gly Ala Ala Ala Phe Lys Ser Val Arg Arg Ala Pro Ala Val Val Ser Pro Arg Ala Val Ser Asp Ser Arg Asn Ser 25 Gln Thr Cys Leu Asp Pro Asp Ala Ser Arg Ser Val Leu Gly Ile Ile Leu Gly Gly Gly Ala Gly Thr Arg Leu Tyr Pro Leu Thr Lys Lys Arg 55 60 Ala Lys Pro Ala Val Pro Leu Gly Ala Asn Tyr Arg Leu Ile Asp Ile 70 Pro Val Ser Asn Cys Leu Asn Ser Asn Val Ser Lys Ile Tyr Val Leu 90 Thr Gln Phe Asn Ser Ala Ser Leu Asn Arg His Leu Ser Arg Ala Tyr 100 105

Ala Ser Asn Met Gly Gly Tyr Lys Asn Glu Gly Phe Val Glu Val Leu 115 120 125

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Ala Ala Gln Gln Ser Pro Glu Asn Pro Asn Trp Phe Gln Gly Thr Ala
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Asp Ala
145
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      <211> 84
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Glu Leu Thr Ala Met Asp Ser Arg Cys Val Ala Leu Lys Ala Asn Ala
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Ser Leu Ala Gln Ser Asn Lys Ser Cys Leu Lys Asn Val Asp Lys Gly
                                25
Phe Leu Gly Glu Arg Ile Arg Gly Ser Leu Asp Asn Ser Val Trp Val
Lys Gln Val Ala Arg Asn Leu Arg Val Glu Lys Lys Phe Lys Lys Ala
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Lys Pro Gly Val Ala Phe Ala Val Ile Thr Ser Asn Thr Val Ala Glu
Thr Leu Thr Ile
      <210> 87
      <211> 113
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      <213> Eucalyptus grandis
      <400> 87
Lys Ile Phe Ile Leu Thr Gln Phe Asn Ser Phe Ser Leu Asn Arg His
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Leu Ser Arg Thr Tyr Asn Phe Asp Asn Gly Val Ser Phe Gly Asp Gly
Phe Val Glu Val Leu Ala Ala Thr Gln Thr Pro Gly Glu Ala Gly Lys
                            40
Arg Trp Phe Gln Gly Thr Ala Asp Ala Val Arg Gln Phe Ile Trp Val
                        55
Phe Glu Asp Ala Lys Asn Lys Asn Val Glu Asn Ile Leu Ile Leu Ser
Gly Asp His Leu Tyr Arg Met Asn Tyr Met Asp Phe Val Gln Lys His
                                    90
Ile Asp Ser Asn Ala Asp Ile Thr Val Ser Cys Val Pro Met Asp Asp
            100
Ser
      <210> 88
      <211> 131
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Ala Ile Ser Val Ala Cys Thr Pro Val Gly Glu Ser Arg Ala Ser Asp
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                                    10
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Tyr Gly Leu Val Lys Ile Asp Ser Arg Gly Gln Ile Val Gln Phe Ser
Glu Lys Pro Lys Gly Pro Asp Leu Thr Ala Met Gln Val Asp Thr Thr
Thr Leu Gly Leu Ser Pro Gln Glu Ala Ala Arg Ser Pro Tyr Ile Ala
Ser Met Gly Val Tyr Ala Phe Lys Thr Glu Ser Leu Leu Asn Leu Leu
Lys Trp Arg Tyr Pro Thr Ala Asn Asp Phe Gly Ser Glu Ile Ile Pro
                                    90
Ser Ala Val Met Glu Gln Asp Val Gln Ala Tyr Ile Phe Arg Asp Tyr
                                105
Trp Glu Asp Ile Gly Thr Ile Lys Ser Phe Tyr Asp Ala Asn Leu Ala
                            120
Leu Thr Glu
    130
      <210> 89
      <211> 115
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      <213> Eucalyptus grandis
      <400> 89
Arg Leu Ser Ser Lys Phe Ile Trp Val Trp Leu Leu Leu Arg Trp Val
Arg Phe Val Gly Met Asp Ser Cys Phe Ala Ser Met Lys Val Gly Ala
Arg Pro Val Pro Gly Gly Gly Ile Ile Asn Phe Ser Glu Phe Trp Gly
Glu Asn Leu Arg Val Gly Ala Asn Lys Gln Phe Gly Ala Arg Leu Cys
                        55
Lys Ser Leu Arg Ser Glu Thr Arg Ile Gly Arg Val Lys Pro Gly Ile
                    70
Ala Tyr Ser Val Leu Thr Pro Glu Val Asp Lys Glu Thr Met Thr Leu
                                    90
Gln Ala Pro Val Leu Glu Thr Pro Arg Ala Asp Pro Lys Ser Phe Ala
                                105
Ser Ile Ile
        115
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      <211> 600
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      <213> Eucalyptus grandis
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Pro Gly Met Ile Gln Val Tyr Leu Gly Ser Ala Gly Ala Leu Asp Val
Glu Gly Lys Glu Leu Pro Arg Leu Val Tyr Val Ser Arg Glu Lys Arg
Pro Gly Tyr Gln His His Lys Lys Ala Gly Ala Met Asn Ala Leu Val
                            40
Arg Val Ser Ala Val Leu Thr Asn Ala Pro Phe Leu Leu Asn Leu Asp
Cys Asp His Tyr Ile Asn Asn Ser Lys Ala Ile Arg Glu Ala Met Cys
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Phe Leu Met Asp Pro Gln Leu Gly Lys Lys Leu Cys Tyr Val Gln Phe

				85					90					95	
Pro	Gln	Arg	Phe 100	Asp	Gly	Ile	Asp	Arg	His	Asp	Arg	Tyr	Ala 110	Asn	Arg
Asn	Ile	Val 115	Phe	Phe	Asp	Ile	Asn 120	Met		Gly	Leu	Asp 125	Gly		Gln
	130					135					140				Leu
145			Asp		150					155					160
			Pro	165					170					175	_
			Lys 180					185					190		
		195	Lys				200					205		_	-
	210		Val			215					220				=
225			Leu		230					235					240
			Gly	245					250					255	Glu
			Leu 260					265					270		
		275	Val				280					285			_
	290		Gly			295					300				
305			Met		310					315					320
			Ala	325					330					335	_
			Val 340					345					350		
		355	Cys				360					365			
	370		Leu Leu			375					380				
385					390					395					400
			Ile	405					410					415	
			Phe 420					425					430	•	_
		435	Val				440					445			
	450		Gly			455					460				
465			Leu		470					475					480
			Asp	485					490					495	
			Ile 500					505					510		-
		515	Gly				520					525			
стХ	530	ьeu	Phe	σīλ		Leu 535	ьvе	Phe	Ala	Phe	Trp 540	Val	Ile	Val	His

Leu Tyr Pro Phe Leu Lys Gly Leu Met Gly Lys Gln Asn Arg Thr Pro 550 555 Thr Ile Val Val Leu Trp Ser Val Leu Leu Ala Ser Ile Phe Ser Leu 565 570 Val Trp Val Arg Ile Asp Pro Phe Leu Pro Lys Gln Thr Gly Pro Val 580 585 Leu Lys Pro Cys Gly Val Glu Cys 595 <210> 91 <211> 222 <212> PRT <213> Pinus radiata <400> 91 Pro Asn Glu Phe Pro Leu Tyr Thr Thr Leu Glu Lys Lys Ser Leu Leu Tyr Arg Ala Tyr Ser Cys Thr His Phe Cys Ala Ile Ile Gly Leu Ile 25 Cys Tyr Arg Leu Leu Tyr Ile Pro Ser Glu Asp Ser Trp Ser Trp Ile Leu Ile Phe Val Ala Glu Leu Gly Phe Ser Tyr Ser Trp Ile Leu Asp 55 Gln Ala Leu Arg Trp Trp Pro Val Gln Arg Thr Val Phe Pro Lys Arg 70 75 Leu Ser Lys Arg Phe Gln Ser Asn Leu Pro Pro Val Asp Ile Phe Ile 85 Cys Thr Ala Asp Pro Phe Lys Glu Pro Pro Leu Thr Val Ile Asn Thr 105 Val Leu Ser Ala Leu Ala Val His Tyr Pro Met Gly Lys Leu Ser Cys 120 125 Tyr Val Ser Asp Asp Gly Gly Ser Pro Leu Thr Phe Tyr Ala Leu Leu 135 140 Glu Ala Ser Arg Phe Ala Lys Ile Trp Ile Pro Phe Cys Asp Lys Tyr 150 155 Ser Ile Glu Asp Arg Cys Pro Glu Val Tyr Phe Ser Asn Pro Ser Ala 165 170 Leu Glu Asn Val Asn Leu Ser Phe Met Thr Asp Trp Arg His Val Asn 185 Lys Met Tyr Phe Glu Leu Lys Asp Arg Ile Asn Asn Val Met Glu Met 200 Gly Ser Val His Gln Ile Asn Arg Met Asn Thr Lys Asp Ser 210 <210> 92 <211> 121 <212> PRT <213> Pinus radiata <400> 92 Ser Lys Leu Leu Met Glu Pro Asn Asp Phe Pro Leu Tyr Thr Thr Leu Glu Lys Lys Ser Leu Leu Tyr Arg Ala Tyr Ser Cys Thr His Phe Ser 20 Ala Ile Ile Gly Leu Ile Cys Tyr Arg Leu Leu Tyr Ile Pro Ser Glu 40 Asp Ser Trp Pro Trp Ile Leu Ile Phe Val Ala Glu Leu Gly Phe Ser

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55
 Tyr Ser Trp Ile Leu Asp Gln Ala Leu Arg Trp Trp Pro Val Glu Arg
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                                         75
 Thr Val Phe Pro Asn Arg Leu Ser Lys Arg Phe Gln Ser Lys Leu Pro
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Pro Val Asp Ile Phe Ile Cys Thr Ala Asp Pro Phe Lys Glu Pro Pro
Leu Thr Val Ile Asn Thr Val Leu Ser
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      <211> 603
      <212> PRT
      <213> Pinus radiata
      <400> 93
Leu Lys Phe Phe Glu Phe Gly Arg Glu Leu Asn Leu Thr Met Glu Ala
Ser Ala Gly Leu Val Ala Gly Ser His Asn Arg Asn Glu Phe Val Val
                                25
Ile His Gly His Glu Glu Pro Lys Pro Leu Asn Thr Leu Ser Gly His
                            40
Val Cys Gln Ile Cys Gly Glu Asp Val Gly Leu Asn Thr Asp Gly Glu
Leu Phe Val Ala Cys Asn Glu Cys Gly Phe Pro Val Cys Arg Pro Cys
                    70
Tyr Glu Tyr Glu Arg Arg Glu Gly Asn Gln Ser Cys Pro Gln Cys Asn
Thr Arg Tyr Lys Arg Gln Lys Gly Ser Pro Arg Val Glu Gly Asp Asp
Asp Glu Glu Asp Val Asp Asp Ile Glu His Glu Phe Asn Val Glu Thr
                            120
Gln Gln Arg Asn Arg Gln Gln Ile Thr Glu Ala Met Leu His Gly Arg
                        135
                                            140
Met Ser Tyr Gly Arg Gly Pro Asp Asp Glu Asn Ser Gln Ile Ala His
                    150
                                        155
Asn Pro Glu Leu Pro Pro Gln Ile Pro Val Leu Ala Asn Gly His Ser
                165
                                    170
Val Val Ser Gly Glu Ile Pro Thr Ser Tyr Tyr Ala Asp Asn Gln Leu
                                185
Leu Ala Asn Pro Ala Met Leu Lys Arg Val His Pro Ser Ser Glu Pro
                                                205
Gly Ser Gly Arg Ile Ile Met Asp Pro Asn Arg Asp Ile Gly Ser Tyr
                        215
Gly Phe Gly Asn Val Ser Trp Lys Glu Arg Gly Asp Gly Tyr Lys Ser
                   230
                                        235
Lys Glu Asn Lys Ser Gly Gln Leu Asp Met Thr Glu Gly Arg Tyr Gln
                245
                                    250
Tyr Asn Gly Gly Phe Ala Pro Asn Glu Pro Glu Asp Tyr Ile Asp Pro
            260
                                265
Asp Met Pro Met Thr Asp Glu Ala Arg Gln Pro Leu Ser Arg Lys Val
                            280
Pro Ile Pro Ser Ser Lys Ile Asn Pro Tyr Arg Met Val Ile Val Ile
                        295
Arg Leu Ile Val Leu Gly Ile Phe Leu Arg Tyr Arg Leu Leu Asn Pro
                                        315
Val Lys Asn Ala Tyr Gly Leu Trp Ala Thr Ser Ile Val Cys Glu Ile
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325 330 Trp Phe Ala Leu Ser Trp Ile Leu Asp Gln Phe Pro Lys Trp Leu Pro 340 345 Ile Ser Arg Glu Thr Tyr Leu Asp Arg Leu Ser Leu Arg Tyr Glu Arg 360 Glu Gly Glu Pro Ser Met Leu Ala Pro Val Asp Leu Phe Val Ser Thr 375 -380 Val Asp Pro Leu Lys Glu Pro Pro Leu Val Thr Ala Asn Thr Val Leu 390 395 Ser Ile Leu Ser Val Asp Tyr Pro Val Asp Asn Val Ser Cys Tyr Val 405 410 Ser Asp Asp Gly Ala Ser Met Leu Thr Phe Glu Ser Leu Ser Glu Thr 420 425 Ser Glu Phe Ala Arg Lys Trp Val Pro Phe Cys Lys Lys Phe Asp Ile 440 Glu Pro Arg Ala Pro Glu Ile Tyr Phe Ser Gln Lys Ile Asp Tyr Leu Lys Asp Lys Phe Gln Pro Thr Phe Val Lys Glu Arg Arg Ala Met Lys 470 475 Arg Glu Tyr Glu Glu Phe Lys Val Arg Ile Asn Arg Leu Val Ala Lys 490 Ala Ser Lys Val Pro Lys Glu Gly Trp Thr Met Gln Asp Gly Thr Pro 505 Trp Pro Gly Asn Asn Thr Arg Asp His Pro Gly Met Ile Gln Val Phe 520 Leu Gly His Ser Gly Gly Leu Asp Thr Glu Gly Asn Glu Leu Pro Arg 535 Leu Val Tyr Val Ser Arg Glu Lys Arg Pro Gly Phe Gln His His Lys 550 555 Lys Ala Gly Ala Met Asn Ala Leu Val Arg Val Ser Ala Val Leu Thr 565 570 Asn Ala Pro Phe Met Leu Asn Leu Asp Cys Asp His Tyr Ile Asn Asn 585 Ser Lys Ala Ile Arg Glu Gly Met Cys Phe Met 595 <210> 94 <211> 245 <212> PRT <213> Pinus radiata Asn His Ile Lys Leu Leu Pro Phe Ala Gln Glu Gln Asn Asp Glu Ile Met Glu Ala Arg Ala Gly Leu Val Ala Gly Ser Tyr Lys Arg Asn Glu Leu Met Val Val Pro Gly His Asp Gly Pro Lys Pro Ile Arg Leu Ser 40 Thr Leu Gln Asp Cys Gln Val Cys Gly Asp Lys Ile Gly Cys Asn Pro

Asn Gly Glu Leu Phe Val Ala Cys Asn Glu Cys Gly Phe Pro Val Cys

Arg Pro Cys Tyr Glu Tyr Glu Arg Lys Asp Gly Asn Arg Cys Cys Pro

Gln Cys Lys Thr Arg Tyr Arg Arg His Lys Gly Ser Pro Arg Val Glu 100 105 110 Gly Asp Asp Glu Glu Asp Gly Met Asp Asp Leu Glu Glu Glu Phe Asn

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115
                            120
Met Glu Arg Asp Arg Gln Ser Val Val Ser His Arg Gly Asn Ala Phe
                       135
Asp Ala Thr Pro Arg Ala Ala His Ser Ile Ala Asn Arg Ser Ile Asn
                    150
                                        155
Gly Asp Asn Tyr Ala Leu Ser Leu Pro Pro Ile Met Asp Gly Asp Ser
                                    170
Leu Ser Val Gln Arg Phe Pro His Ala Ala Thr Val Ile Gly Asn Gly
                                185
Leu Asp Pro Val Lys Glu Asn Tyr Gly Ser Ala Ala Trp Lys Glu Arg
                            200
Val Glu Asn Trp Lys Ala Lys His Asp Lys Lys Ser Gly Ser Ile Lys
                        215
                                            220
Asp Gly Ile Tyr Asp Pro Asp Glu Ala Asp Asp Ile Met Met Thr Glu
                                        235
Ala Glu Ala Arg Gln
                245
      <210> 95
      <211> 149
      <212> PRT
      <213> Eucalyptus grandis
      <400> 95
Leu Glu Arg Val Ser Gly Thr Glu His Ser His Ile Leu Arg Val Pro
Phe Arg Ser Asp Gln Gly Ile Leu Arg Lys Trp Ile Ser Arg Phe Asp
                                25
Val Trp Pro Tyr Leu Glu Thr Phe Ala Leu Asp Ala Ala His Glu Ile
Thr Ala Glu Leu Gln Gly Phe Pro Asp Phe Ile Ile Gly Asn Tyr Ser
                        55
Asp Gly Asn Leu Val Ala Ser Leu Leu Ala Tyr Lys Met Gly Val Thr
                    70
Gln Cys Thr Ile Ala His Ala Leu Glu Lys Thr Lys Tyr Pro Asp Ser
                                    90
Asp Ile Tyr Trp Lys Lys Phe Asp Glu Lys Tyr His Phe Ser Cys Gln
                                105
Phe Thr Ala Asp Leu Leu Ala Met Asn Asn Ala Asp Phe Ile Ile Thr
                            120
Ser Thr Tyr Gln Glu Ile Ala Gly Thr Lys Asn Thr Val Gly Gln Tyr
Glu Ser His Thr Ala
145
      <210> 96
      <211> 124
      <212> PRT
      <213> Eucalyptus grandis
      <400> 96
Leu Ala Lys Ala Gly Thr Lys Asn Thr Val Gly Gln Tyr Glu Ser His
Thr Ala Phe Thr Leu Pro Gly Leu Tyr Arg Val Val His Gly Ile Asp
Val Phe Asp Pro Lys Phe Asn Ile Val Ser Pro Gly Ala Asp Met Cys
                            40
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Ile Tyr Phe Pro Tyr Ser Glu Lys Gln Lys Arg Leu Thr Ala Leu His
Gly Ser Ile Glu Lys Leu Leu Tyr Asp Pro Glu Gln Asn Asp Glu His
Ile Gly Ser Leu Ser Asp Arg Ser Lys Pro Met Ile Phe Ser Met Ala
                                     90
Arg Leu Asp Lys Val Lys Asn Met Thr Gly Leu Val Glu Cys Tyr Ala
                                105
Lys Asn Ser Lys Leu Arg Glu Leu Ala Asn Leu Val
      <210> 97
      <211> 61
      <212> PRT
      <213> Eucalyptus grandis
      <400> 97
Glu Ala Ile Val Leu Pro Pro Phe Val Ala Ile Ala Val Arg Pro Arg
Pro Gly Val Trp Glu Tyr Val Arg Val Asn Val His Glu Leu Ser Val
Glu Gln Leu Thr Val Ser Glu Tyr Leu Gly Phe Lys Glu Glu Leu Val
                            40
Asp Gly Lys Ser Glu Asp Ser Phe Val Leu Glu Leu Asp
                        55
      <210> 98
      <211> 217
      <212> PRT
      <213> Pinus radiata
      <400> 98
Cys Val Gly Ile Asp Pro Lys Ala Asn Met Val Ser Ala Arg Leu Thr
                                    10
Arg Ser Leu Ser Ser Arg Glu Arg Val Glu Asp Thr Leu Ser Glu His
                                25
Arg Asn Gln Leu Ala Ala Leu Phe Ser Arg Tyr Val Ala Gln Gly Lys
Lys Val Leu Gln Pro His Glu Ile Leu Asp Gly Leu Ala Ala Val Ile
                        55
Gly Glu Asn Asp Glu His Gln Asn Phe Arg Asp Gly Leu Phe Gly Asn
Val Leu Arg Ser Thr Gln Glu Ala Ile Ile Ile Pro Pro Trp Val Val
                85
                                    90
Leu Ala Val Arg Pro Arg Pro Gly Val Trp Glu Phe Val Arg Val Asn
                                105
Val Asp Glu Leu Ala Val Glu Gln Leu Ser Val Ala Glu Tyr Leu Glu
Phe Lys Glu Gln Leu Val Asp Gly Ser Val Lys Asp Asn Tyr Val Leu
                        135
Glu Leu Asp Leu Glu Pro Phe Asn Ala Ser Phe Pro Arg Pro Thr Gln
                    150
                                        155
Pro Ser Ser Ile Gly Ser Gly Val Gln Phe Leu Asn Arg His Leu Ser
                                    170
Ser Arg Leu Phe Arg Asp His Glu Ser Met Gln Pro Leu Leu Asp Phe
                                185
Leu Arg Ala His Lys Tyr Gln Gly Gln Arg Leu Met Leu Asn Glu Arg
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195
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                                                205
Ile Gln Ser Leu Thr Lys Leu Arg Ser
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      <211> 348
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      <213> Pinus radiata
      <400> 99
Gly Thr Lys Ser Trp Ser Ser Arg Ala Cys Arg Ser Thr Leu Val Asp
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Pro Lys Asn Ser Ala Arg Asp Gly Ile Asp Val Phe Asp Pro Lys Phe
                                25
Asn Ile Val Ser Pro Gly Ala Asp Met Gln Ile Tyr Phe Pro Tyr Thr
Glu Lys Gln His Arg Leu Thr Thr Leu His Gly Thr Ile Glu Glu Leu
                        55
Leu Phe Ser Pro Glu Gln Thr Ala Glu His Met Cys Ala Leu Asn Asp
                    70
                                        75
Arg Lys Lys Pro Ile Ile Phe Ser Met Ala Arg Leu Asp Arg Val Lys
                                    90
Asn Met Thr Gly Leu Val Glu Trp Phe Ala Lys Ser Lys Arg Leu Arg
            100
                                105
Glu Leu Val Asn Leu Val Val Val Ala Gly Asp Ile Asp Pro Ser Lys
                            120
Ser Lys Asp Arg Glu Glu Val Ala Glu Ile Glu Lys Met His Arg Leu
Val Lys Glu Tyr Asn Leu Asn Gly Gln Phe Arg Trp Ile Cys Ala Gln
                   150
                                       155
Lys Asn Arg Val Arg Asn Gly Glu Leu Tyr Arg Tyr Ile Cys Asp Thr
                                    170
Arg Gly Ala Phe Val Gln Pro Ala Leu Tyr Glu Ala Phe Gly Leu Thr
            180
                                185
Val Val Glu Ala Met Thr Cys Gly Leu Pro Thr Phe Ala Thr Cys Asn
                            200
Gly Gly Pro Ala Glu Ile Ile Val Asp Gly Val Ser Gly Phe His Ile
                        215
                                            220
Asp Pro Tyr His Gly Val Ser Ala Thr Glu Arg Ile Ala Asp Phe Phe
                    230
                                        235
Glu Lys Cys Lys Thr Asp Pro Ser His Trp Glu Lys Ile Ser Asn Gly
                245
                                   250
Gly Leu Gln Arg Ile Tyr Glu Lys Tyr Thr Trp Gln Ile Tyr Ala Asp
                               265
Arg Leu Met Thr Leu Ser Gly Val Tyr Gly Phe Trp Lys Tyr Val Ser
                            280
Lys Leu Glu Arg Arg Glu Thr Arg Arg Tyr Leu Glu Met Phe Tyr Ser
                        295
                                            300
Leu Lys Tyr Arg Asn Leu Val Lys Thr Val Pro Leu Ala Val Glu Glu
                                       315
Ser Val Asn Gly Ile Glu Glu Lys Ser Thr Glu Phe Arg Trp Leu His
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Ser Cys Arg Ser Cys Arg Pro Arg His Phe Ala Gln
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      <211> 139
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<212> PRT <213> Pinus radiata <400> 100 Ser Asn Leu Glu Thr Phe Leu Gly Arg Val Pro Met Val Phe Asn Val Val Ile Leu Ser Pro His Gly Tyr Phe Gly Gln Ala Asn Val Leu Gly Met Pro Asp Thr Gly Gly Gln Val Val Tyr Ile Leu Asp Gln Cys Arg Ala Leu Glu Asn Glu Met Leu Leu Arg Ile Lys Gln Gln Gly Leu Asp 55 Ile Thr Pro Glu Ile Ile Val Val Thr Arg Leu Ile Pro Glu Ala His Gly Thr Thr Cys Asn Gln Arg Leu Glu Lys Ile Ser Gly Thr Gln His Ser Arg Ile Leu Arg Val Pro Phe Arg Thr Glu Lys Gly Val Val Arg 105 Asp Trp Val Ser Arg Phe Asp Val Trp Pro Tyr Leu Glu Arg Phe Ser 120 Glu Asp Val Thr Asn Glu Ile Ala Val Glu Leu 130 135 <210> 101 <211> 68 <212> PRT <213> Pinus radiata <400> 101 Ile Leu Leu Ile Val Gly Ile Gly Ile His Ile Lys Ala Lys Glu Asn Met Val Ala Ala Ala Leu Thr His Ala Leu Ser Ser Arg Glu Arg 25 Val Glu Asp Met Leu Ser Glu His Arg Asn Glu Ile Val Ser Leu Leu 40 Ser Arg Tyr Val Ala Glu Gly Lys Lys Ile Leu Gln Pro His Gln Leu 55 Leu Asp Gly Leu 65 <210> 102 <211> 70 <212> PRT <213> Eucalyptus grandis <400> 102 Met Ala Ala Pro Lys Leu Gly Arg Ile Pro Ser Ile Arg Asp Arg Val Glu Asp Thr Leu Ala Ala His Arg Asn Glu Leu Val Ser Leu Leu Ser - 25 Arg Tyr Val Ala Gln Gly Lys Gly Ile Leu Gln Pro His His Leu Leu 40 Asp Glu Leu Glu Asn Ile Ile Ser Glu Asp Glu Gly Lys Ser Ser Leu Ser Asp Gly Pro Phe Ser

<210> 103 <211> 534 <212> PRT <213> Eucalyptus grandis <400> 103 Val Leu Phe Thr His Leu Pro Pro Gln Lys Pro Asn Arg Ile Ser Leu 10 Leu Leu Phe Phe Ile Phe His Ile Thr Thr Phe Leu Leu Leu Leu Leu Leu Ser Val Leu Ser Thr Phe Ile Ser Ile Ala Val Ser Leu Ser 40 Asp Pro Glu Leu Phe Phe Ala Ser Pro Pro Met Ala Ala Ala Thr 55 60 Leu Ser Ala Pro Asp Ala Ala Lys Leu Ser Gln Leu Lys Ser Ala Val 70 75 Ser Gly Leu Gly Gln Ile Ser Glu Ser Glu Lys Asn Gly Phe Ile Asn 90 Leu Val Ser Arg Tyr Leu Ser Gly Glu Ala Gln His Val Asp Trp Ser 105 Lys Ile Gln Thr Pro Thr Asp Glu Ile Val Val Pro Tyr Asp Ser Leu 120 125 Ala Pro Thr Pro Gln Asp Pro Ala Ala Thr Lys Ser Leu Leu Asp Lys 135 140 Leu Val Val Leu Lys Leu Asn Gly Gly Leu Gly Thr Thr Met Gly Cys 150 155 Thr Gly Pro Lys Ser Val Ile Glu Val Arg Asn Gly Leu Thr Phe Leu 170 Asp Leu Ile Val Ile Gln Ile Glu Asn Leu Asn Thr Lys Tyr Gly Cys 180 185 Asn Val Pro Leu Leu Met Asn Ser Phe Asn Thr His Asp Asp Thr 200 Leu Lys Ile Val Glu Lys Tyr Ala Asn Ser Asn Ile Asp Ile His Thr 215 220 Phe Asn Gln Ser Gln Tyr Pro Arg Leu Val Val Glu Asp Phe Met Pro 230 235 Leu Pro Cys Lys Gly Gln Thr Gly Lys Asp Gly Trp Tyr Pro Pro Gly 245 250 His Gly Asp Val Phe Ala Ser Leu Met Asn Ser Gly Lys Leu Asp Ala 265 Leu Leu Ser Gln Gly Lys Glu Tyr Val Phe Ala Ala Asn Ser Asp Asn 280 Leu Gly Ala Ile Val Asp Leu Lys Ile Leu Asn His Leu Met Thr Asn 295 Lys Asn Glu Tyr Cys Met Glu Val Thr Pro Lys Thr Leu Ala Asp Val 310 315 Lys Gly Gly Thr Leu Ile Ser Tyr Glu Gly Lys Val Gln Leu Leu Glu 325 330 Ile Ala Gln Val Pro Asp Glu His Ile Asn Glu Phe Lys Ser Ile Glu 345 Lys Phe Lys Ile Phe Asn Thr Asn Asn Leu Trp Val Asn Leu Lys Ala 360 Ile Lys Arg Leu Val Glu Ala Gln Ala Leu Lys Met Glu Ile Ile Pro 375 Asn Pro Lys Glu Val Asp Gly Ile Lys Val Leu Gln Leu Glu Thr Ala 395 Ala Gly Ala Ala Ile Lys Phe Phe Asp Asn Ala Ile Gly Ile Asn Val

405 410 Pro Arg Ser Arg Phe Leu Pro Val Lys Ala Thr Ser Asp Leu Leu 425 420 Val Gln Ser Asp Leu Tyr Thr Leu Val Asp Gly Phe Val Glu Arg Asn 440 Lys Ala Arg Thr Asn Pro Ser Asn Pro Ser Ile Glu Leu Gly Pro Glu 455 Phe Lys Lys Val Gly Asn Phe Leu Ser Arg Phe Lys Ser Ile Pro Ser 470 475 Ile Ile Glu Leu Asp Ser Leu Lys Val Ser Gly Asp Val Trp Phe Gly 485 490 Thr Gly Ile Thr Leu Lys Gly Lys Val Thr Ile Ala Ala Lys Pro Gly 505 Val Lys Leu Glu Ile Pro Asp Gly Val Val Leu Glu Asn Lys Glu Ile 520 His Gly Pro Glu Asp Leu 530 <210> 104 <211> 480 <212> PRT <213> Pinus radiata <400> 104 Met Ala Ala Pro Ala Val Ala Ser Pro Ala Ala Glu Thr Asp Arg Ile Pro Lys Leu Gln Ala Glu Val Thr Lys Leu Asn Gln Ile Ser Asp Asn Glu Lys Glu Gly Phe Val Arg Leu Val Ser Arg Tyr Leu Ser Gly 40 Glu Glu Lys Ile Glu Trp Glu Lys Ile Lys Thr Pro Thr Asp Glu Ile Val Val Pro Tyr Asp Thr Leu Ala Ala Leu Gly Glu Asp Pro Ser 75 Glu Thr Lys Glu Leu Leu Asp Lys Leu Val Val Leu Lys Leu Asn Gly 85 90 Gly Leu Gly Thr Thr Met Gly Cys Thr Gly Pro Lys Ser Val Ile Glu 105 Val Arg Asn Gly Leu Thr Phe Leu Asp Leu Ile Val Lys Gln Ile Glu Ser Leu Asn Asn Lys Tyr Asp Ser Lys Val Pro Leu Val Leu Met Asn 135 Ser Phe Asn Thr His Asp Asp Thr Ile Lys Ile Val Glu Lys Tyr Ser 150 155 Gly Ser Asn Ile Asp Ile His Ile Phe Asn Gln Ser Gln Tyr Pro Arg 165 170 Met Val Ala Glu Asp Leu Thr Pro Trp Pro Thr Lys Gly Arg Thr Asp 180 185 Lys Glu Ala Trp Tyr Pro Pro Gly His Gly Asp Val Phe Pro Ala Leu 200 Leu Asn Ser Gly Lys Leu Asp Glu Leu Leu Ser Gln Gly Lys Glu Tyr 215 Val Phe Ile Ala Asn Ser Asp Asn Leu Gly Ala Ile Val Asp Leu Lys 230 235 Ile Leu Asn His Leu Val Lys Asn Lys Asn Glu Tyr Cys Met Glu Val 245 250 Thr Pro Lys Thr Leu Ala Asp Val Lys Gly Gly Thr Leu Ile Ser Tyr

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260
                                265
Glu Gly Arg Val Gln Leu Leu Glu Ile Ala Gln Val Pro Glu Glu His
                            280
Val Gly Glu Phe Lys Ser Ile Glu Lys Phe Lys Ile Phe Asn Thr Asn
Asn Leu Trp Val Asn Leu Lys Ala Ile Lys Arg Leu Val Glu Ala Asp
                    310
                                        315
Ala Leu Lys Met Glu Ile Ile Pro Asn Pro Lys Glu Val Asp Gly Val
                                    330
Lys Val Leu Gln Leu Glu Thr Ala Ala Gly Ala Ala Ile Arg Phe Phe
                                345
Asp Arg Ala Ile Gly Val Asn Val Pro Arg Ser Arg Phe Leu Pro Val
        355
                            360
Lys Ala Thr Ser Asp Leu Leu Leu Val Gln Ser Asp Leu Tyr Thr Val
                        375
Glu Glu Gly Phe Val Ile Arg Asn Pro Ala Arg Val Asn Pro Thr Asn
                                        395
Pro Thr Ile Glu Leu Gly Pro Glu Phe Lys Lys Val Gly Asn Phe Leu
                405
                                    410
Lys Arg Phe Lys Ser Ile Pro Ser Ile Ile Asp Leu Asp Ser Leu Lys
            420
                                425
Val Ser Gly Asp Val Trp Phe Gly Ser Gly Val Ile Leu Lys Gly Lys
                            440
Val Ile Ile Glu Ala Lys Gln Gly Ala Thr Leu Glu Ile Pro Asp Glu
                        455
                                            460
Ser Val Ile Glu Asn Lys Val Val Ser Ser Pro Asp Asp Ile Val Asn
                    470
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<210> 105

<211> 573

<212> DNA

<213> Eucalyptus grandis

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                                                                       60
aaagggcctc ccccattcct catttttcac catcctccgt tcgttcgttc ccttcccttt
                                                                       120
ccattgttgc gtttaagccc tccaattttc ttttggcgtc ccgtttttgg ggctcccttg
                                                                       180
aagatctcct cttcatttcg ggatttcctg ccttcgccgc gccatttgaa gttctttttc
                                                                       240
tgagagaaga atttagacat ggctgatcgc atgctgactc gaagccacag ccttcgcgag
                                                                       300
cgtttggacg agaccctctc tgctcaccgc aacgatattg tggccttcct ttcaagggtt
                                                                       360
gaagccaagg gcaaaggcat cttgcagcgc caccagattt ttgctgagtt tgaggccatc
                                                                       420
tctgaggaga gcagagcaaa gcttcttgat ggggcctttg gtgaagtcct caaatccact
                                                                       480
caggaagcga ttgtgtcgcc tccatgggtt gctcttgctg ttcgtccaag gccgggcgtg
                                                                       540
tgggagcaca tccgtgtgaa cgtccatgcg ctt
                                                                       573
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<210> 106

<211> 105

<212> PRT

<213> Eucalyptus grandis

<400> 106

Met Ala Asp Arg Met Leu Thr Arg Ser His Ser Leu Arg Glu Arg Leu

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7
                                     10
Asp Glu Thr Leu Ser Ala His Arg Asn Asp Ile Val Ala Phe Leu Ser
                                 25
Arg Val Glu Ala Lys Gly Lys Gly Ile Leu Gln Arg His Gln Ile Phe
                             40
Ala Glu Phe Glu Ala Ile Ser Glu Glu Ser Arg Ala Lys Leu Leu Asp
Gly Ala Phe Gly Glu Val Leu Lys Ser Thr Gln Glu Ala Ile Val Ser
                                         75
Pro Pro Trp Val Ala Leu Ala Val Arg Pro Arg Pro Gly Val Trp Glu
                85
His Ile Arg Val Asn Val His Ala Leu
            100
      <210> 107
      <211> 664
      <212> DNA
      <213> Eucalyptus grandis
      <400> 107
ggcacgagct cttctcgtct cgctttctca tataaagaag tgaaagaata cgaggatact
                                                                        60
ccacttgggt atcgccaaga actcattggg tcgcgagaag attggccaac atgatggaat
                                                                       120
ccggggttcc cctgtgcaac acttgcggag aggctgttgg ggttgatgag aaaggcgagg
                                                                       180
tettegtgge ttgtcaagag tgcaactteg ccatttgcaa ggettgtgte gaatatgaga
                                                                       240
ttaaggaagg aagaaaagcg tgcttgcgct gtggcactcc atttgaagcg aactcgatgg
                                                                       300
ctgatgctga gagaaatgaa ttgggaagtc gatcgacaat ggcagctcaa ctcaatgatc
                                                                       360
ctcaggacac agggattcat gctagacaca tcagcagtgt ttctacgttg gatagtgaat
                                                                       420
acaatgatga gactgggaac cctatctgga agaatagagt ggagagctgg aaggacaaaa
                                                                       480
agaataagaa gaagaaggcc ccgacgaagg ctgagaaaga ggctcaagtt ccaccagagc
                                                                       540
agcagatgga agagaagcaa attgctgatg cttcagagcc actctcgacc gttattccca
                                                                       600
ttgccaaaag caaactcgca ccataccgaa ccgtaataat aatgcgattg atcattttgg
                                                                       660
cact
                                                                       664
      <210> 108
      <211> 184
      <212> PRT
      <213> Eucalyptus grandis
      <400> 108
Met Met Glu Ser Gly Val Pro Leu Cys Asn Thr Cys Gly Glu Ala Val
Gly Val Asp Glu Lys Gly Glu Val Phe Val Ala Cys Gln Glu Cys Asn
                                25
Phe Ala Ile Cys Lys Ala Cys Val Glu Tyr Glu Ile Lys Glu Gly Arg
Lys Ala Cys Leu Arg Cys Gly Thr Pro Phe Glu Ala Asn Ser Met Ala
                                            60
Asp Ala Glu Arg Asn Glu Leu Gly Ser Arg Ser Thr Met Ala Ala Gln
                    70
                                        75
Leu Asn Asp Pro Gln Asp Thr Gly Ile His Ala Arg His Ile Ser Ser
                                    90
Val Ser Thr Leu Asp Ser Glu Tyr Asn Asp Glu Thr Gly Asn Pro Ile
                                105
Trp Lys Asn Arg Val Glu Ser Trp Lys Asp Lys Lys Asn Lys Lys
                            120
Lys Ala Pro Thr Lys Ala Glu Lys Glu Ala Gln Val Pro Pro Glu Gln
    130
                        135
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Gln Met Glu Glu Lys Gln Ile Ala Asp Ala Ser Glu Pro Leu Ser Thr
                     150
                                         155
Val Ile Pro Ile Ala Lys Ser Lys Leu Ala Pro Tyr Arg Thr Val Ile
                 165
                                     170.
                                                         175
Ile Met Arg Leu Ile Ile Leu Ala
             180
      <210> 109
      <211> 1293
      <212> DNA
      <213> Pinus radiata
      <400> 109
etgactetet etetetetgt titigteteet eceteetete tetegittite gettegtegt
                                                                         60
quacgcaccc acacgatett ceatteecte aacaatgteg acteteaceg tecegoagee
                                                                        120
actgccccct gtagccgatg actgcgagca gctccggaca gccttcgcag gatggggaac
                                                                        180
aaatgagaag ctgatcatat ccatattggg tcataggaat gcggcgcaga ggaagctgat
                                                                        240
teggeaaace tatgeegaga ettaeggega ggaceteete aaggeattgg acagagaact
                                                                        300
taccaatgat ttcgagaggc tggtggtcct ttggtcactt gatccggctg aacgtgatgc
                                                                        360
gtacttggcg aatgaagcga cgaaaagatg gacttcaagc aaccaggttc tcatggaaat
                                                                        420
agectgeacg aggteteege ageagttget tatggeaaga caageatate atgeeegata
                                                                        480
caagaagtca atggaagagg acgtcgctca ccacacaact ggagattttc gtaagttgct
                                                                        540
ggtacctctt gggagctcct accgtaatga tggagatgag gtgaatatga ctttggcaaa
                                                                        600
agcagagget aagatactee acgagaagat etcagagaag gettatggee atgaggatet
                                                                        660
cataaggatt ttggctacta ggagcaaagc acaggtcaat gctacgctga atcactacaa
                                                                       720
aaatgagttt ggaaatgata tcaacaagga tttgaaaact gatccaaaag acgcgttcct
                                                                        780
tactatactg agagetacag taaagtgeet gactegeeet gagaagtatt ttgaaaaggt
                                                                        840
tettegteta gecateaata agegaggaae agatgaaggg getetgaeea gagtagttge
                                                                       900
taccagggcc gaggttgaca tgaagtttat aagtgaggag taccagagga ggaatagcat
                                                                       960
ccctctcgat cgtgccattg tcaaggacac tactggagac tatgaaaaaa tgcttctggc
                                                                      1020
attgattggc cacgtcgagg cttgatttac aagtactcat gaagctatcc tggtggaggc
                                                                      1080
aatatctctg tttttggtgt ggtttgaggc atttctattt tccttgcttt ccaacaacgt
                                                                      1140
gtagttacca acatgcctcc ccagttgtca gttgtagcta tgcgaagcaa atacacttct
                                                                      1200
tataatggcg ttggtttatg tacttatgag aagtctttga ttttgatctt taatcaagac
                                                                      1260
tgctagtaag tgatcgtgaa aaaaaaaaaa aaa
                                                                      1293
      <210> 110
      <211> 484
      <212> DNA
      <213> Pinus radiata
      <400> 110
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acagagaact taccaatgat tttgaggtct gatcttcttt aattatttgt attcatccca
                                                                       120
tggagacgcg tecetette teteagatta atceatatte atteegtate gteagagget
                                                                       180
ggtggtcctt tggtcgcttg atccggctga acgtgatgcg tacttggcga atgaagcgac
                                                                       240
gaaaagatgg acttcaagca accaggttct catggaaata gcctgcacga ggtctccaca
                                                                       300
gcagttgctc atggcaagac aagcatatca tgctcgatac aagaagtcgc tggaagagga
                                                                       360
cgtcgctcac cacacaactg gagattttcg taagttgctg gtacctcttg tgagctccta
                                                                       420
ccattatgat ggagatgagg tgaatatgac tttggcaaaa gcagaggcta agatactcca
                                                                       480
cgag
                                                                       484
      <210> 111
      <211> 221
      <212> DNA
      <213> Pinus radiata
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<400> 111
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tagcctgcac gaggtctccg cagcagttgc ttatggcaag acaagcatat catgcccgat
                                                                        120
acaagaagtc gctggaagag gacgtcggtc accacacaac tggagatttt cgtaagttgc
                                                                        180
tggtacctct tgtgagctcc taccgttatg atggagatga g
                                                                        221
      <210> 112
      <211> 789
      <212> DNA
      <213> Pinus radiata
      <400> 112
ategtetteg geteetegeg atateaceaa ettgetteeg cacagagaga gagagagaa
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gagagagaga gaatggcgac tatcgcggtg ccaccgtcgg ttccgtctcc ggctgaggat
                                                                       120
gccgagcagc tccaaaaagc tttcgcagga tgggggacga atgaagatct gatcatatcc
                                                                       180
atactgcctc acagaaacgc agcgcagcgg aaagtaatcc gacaaacata tgccgagaca
                                                                       240
tatggggaag atcttctcaa agcgcttgac aaggaactct ctagtgactt tgagagatct
                                                                       300
gtgcttctgt ggaccctgga tcctgcggag cgtgatgcat tcttgtccaa tgaagctacc
                                                                       360
aagagattga cttcgagcaa ctgggttctc atggaaattg cttgcacgag qtcttcaatg
                                                                       420
gagttattca tggtgaggca ggcctatcat gctcgttata agaaatctct tgaagaagac
                                                                       480
ategeatate acactactgg ggattteege aagetgettg tteetetgge aagtacettt
                                                                       540
cggtatgagg ggcctgaggt gaacatgaca ttggcgagat cagaggctaa gatacttcat
                                                                       600
gagaagattc acgagaaggc ttacaatcat gatgagctca tcagaattgt tactacaaqa
                                                                       660
agtaaagete agettaatge aacceteaat tactacaaca atgagtttgg gaatgecate
                                                                       720
aacaaggatc tgaaggctga tccaaatgat gaatttctga aactgctgag atcagcaatt
                                                                       780
aagtgcttg
                                                                       789
      <210> 113
      <211> 704
      <212> DNA
      <213> Pinus radiata
      <400> 113
gttttgttga gctactagat tttagtaaat caagaattca tcagctataa attgaggcat
                                                                        60
tegattteag ttttagttac attttggtga agttggtega cetgcattge tgaagatate
                                                                       120
gtgcgaagta tgtgatttgt cgagaagatg tcaacaatta tagtgccagt tccaataccg
                                                                       180
accccatctg aagactctga acgcctgagg aaggcttttg aagggtgggg cacaaatgag
                                                                       240
aagtcaatca tacaaatatt aggacataga actgcagcac aacgcaaagt aatccgtcaa
                                                                       300
agttattttc aactgtacga agaggatctc ttgaagcgat tagaatctga gctttcaagt
                                                                       360
gactttgaga aagctgtatt cctttgggta ctagatccag ctgaacgtga tgcggtcata
                                                                       420
tctcatggtg caataaagaa gtggaatgca aagaatatat cgcttttaga aatttccagt
                                                                       480
gctcgatctt cggctgaact attgatggtg aggcaagcat atcatattcg gtacaaaaag
                                                                       540
teeetegaag aagaegtgge tgeacataea agtggaaaet teegtaagtt getggtagea
                                                                       600
cttgtaagtt catatcggta tgaaggtccg gaagtggata tgcatttggc aagttatgaa
                                                                       660
gcaaagaagc taagtgaatc tataaccgag caaaaaagat aatt
                                                                       704
      <210> 114
      <211> 316
      <212> PRT
      <213> Pinus radiata
      <400> 114
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1
                 5
                                    10
Cys Glu Gln Leu Arg Thr Ala Phe Ala Gly Trp Gly Thr Asn Glu Lys
                                25
Leu Ile Ile Ser Ile Leu Gly His Arg Asn Ala Ala Gln Arg Lys Leu
```

```
40
 Ile Arg Gln Thr Tyr Ala Glu Thr Tyr Gly Glu Asp Leu Leu Lys Ala
Leu Asp Arg Glu Leu Thr Asn Asp Phe Glu Arg Leu Val Val Leu Trp
Ser Leu Asp Pro Ala Glu Arg Asp Ala Tyr Leu Ala Asn Glu Ala Thr
                                    90
Lys Arg Trp Thr Ser Ser Asn Gln Val Leu Met Glu Ile Ala Cys Thr
                                105
Arg Ser Pro Gln Gln Leu Leu Met Ala Arg Gln Ala Tyr His Ala Arg
                            120
                                                 125
 Tyr Lys Lys Ser Met Glu Glu Asp Val Ala His His Thr Thr Gly Asp
                        135
Phe Arg Lys Leu Leu Val Pro Leu Gly Ser Ser Tyr Arg Asn Asp Gly
                    150
Asp Glu Val Asn Met Thr Leu Ala Lys Ala Glu Ala Lys Ile Leu His
                                     170
Glu Lys Ile Ser Glu Lys Ala Tyr Gly His Glu Asp Leu Ile Arg Ile
Leu Ala Thr Arg Ser Lys Ala Gln Val Asn Ala Thr Leu Asn His Tyr
                            200
Lys Asn Glu Phe Gly Asn Asp Ile Asn Lys Asp Leu Lys Thr Asp Pro
                        215
                                             220
Lys Asp Ala Phe Leu Thr Ile Leu Arg Ala Thr Val Lys Cys Leu Thr
                    230
                                        235
Arg Pro Glu Lys Tyr Phe Glu Lys Val Leu Arg Leu Ala Ile Asn Lys
                245
                                    250
Arg Gly Thr Asp Glu Gly Ala Leu Thr Arg Val Val Ala Thr Arg Ala
                                265
Glu Val Asp Met Lys Phe Ile Ser Glu Glu Tyr Gln Arg Arg Asn Ser
                            280
Ile Pro Leu Asp Arg Ala Ile Val Lys Asp Thr Thr Gly Asp Tyr Glu
                        295
Lys Met Leu Leu Ala Leu Ile Gly His Val Glu Ala
305
      <210> 115
      <211> 111
      <212> PRT
      <213> Pinus radiata
      <400> 115
Ser Ile Phe Ile Pro Tyr Arg Gln Arg Leu Val Val Leu Trp Ser Leu
                                    10
Asp Pro Ala Glu Arg Asp Ala Tyr Leu Ala Asn Glu Ala Thr Lys Arg
Trp Thr Ser Ser Asn Gln Val Leu Met Glu Ile Ala Cys Thr Arg Ser
                            40
Pro Gln Gln Leu Leu Met Ala Arg Gln Ala Tyr His Ala Arg Tyr Lys
Lys Ser Leu Glu Glu Asp Val Ala His His Thr Thr Gly Asp Phe Arg
                    70
Lys Leu Leu Val Pro Leu Val Ser Ser Tyr His Tyr Asp Gly Asp Glu
                                    90
Val Asn Met Thr Leu Ala Lys Ala Glu Ala Lys Ile Leu His Glu
                                105
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<210> 116 <211> 73 <212> PRT <213> Pinus radiata <400> 116 Tyr Leu Ala Asn Glu Ala Thr Lys Arg Trp Thr Ser Ser Asn Gln Val 5 10 Leu Met Glu Ile Ala Cys Thr Arg Ser Pro Gln Gln Leu Leu Met Ala Arg Gln Ala Tyr His Ala Arg Tyr Lys Lys Ser Leu Glu Glu Asp Val 40 Gly His His Thr Thr Gly Asp Phe Arg Lys Leu Leu Val Pro Leu Val 55 Ser Ser Tyr Arg Tyr Asp Gly Asp Glu <210> 117 <211> 239 <212> PRT <213> Pinus radiata <400> 117 Met Ala Thr Ile Ala Val Pro Pro Ser Val Pro Ser Pro Ala Glu Asp 10 Ala Glu Gln Leu Gln Lys Ala Phe Ala Gly Trp Gly Thr Asn Glu Asp Leu Ile Ile Ser Ile Leu Pro His Arg Asn Ala Ala Gln Arg Lys Val Ile Arg Gln Thr Tyr Ala Glu Thr Tyr Gly Glu Asp Leu Leu Lys Ala 55 Leu Asp Lys Glu Leu Ser Ser Asp Phe Glu Arg Ser Val Leu Leu Trp Thr Leu Asp Pro Ala Glu Arg Asp Ala Phe Leu Ser Asn Glu Ala Thr 90 Lys Arg Leu Thr Ser Ser Asn Trp Val Leu Met Glu Ile Ala Cys Thr 105 Arg Ser Ser Met Glu Leu Phe Met Val Arg Gln Ala Tyr His Ala Arg 120 Tyr Lys Lys Ser Leu Glu Glu Asp Ile Ala Tyr His Thr Thr Gly Asp Phe Arg Lys Leu Leu Val Pro Leu Ala Ser Thr Phe Arg Tyr Glu Gly 150 155 Pro Glu Val Asn Met Thr Leu Ala Arg Ser Glu Ala Lys Ile Leu His 170 Glu Lys Ile His Glu Lys Ala Tyr Asn His Asp Glu Leu Ile Arg Ile 185 Val Thr Thr Arg Ser Lys Ala Gln Leu Asn Ala Thr Leu Asn Tyr Tyr 200 Asn Asn Glu Phe Gly Asn Ala Ile Asn Lys Asp Leu Lys Ala Asp Pro 215 220 Asn Asp Glu Phe Leu Lys Leu Leu Arg Ser Ala Ile Lys Cys Leu 230 <210> 118 <211> 184 <212> PRT

## <213> Pinus radiata

<400> 118 Met Ser Thr Ile Ile Val Pro Val Pro Ile Pro Thr Pro Ser Glu Asp Ser Glu Arg Leu Arg Lys Ala Phe Glu Gly Trp Gly Thr Asn Glu Lys Ser Ile Ile Gln Ile Leu Gly His Arg Thr Ala Ala Gln Arg Lys Val Ile Arg Gln Ser Tyr Phe Gln Leu Tyr Glu Glu Asp Leu Leu Lys Arg 55 Leu Glu Ser Glu Leu Ser Ser Asp Phe Glu Lys Ala Val Phe Leu Trp 70 75 Val Leu Asp Pro Ala Glu Arg Asp Ala Val Ile Ser His Gly Ala Ile 85 90 Lys Lys Trp Asn Ala Lys Asn Ile Ser Leu Leu Glu Ile Ser Ser Ala 105 Arg Ser Ser Ala Glu Leu Leu Met Val Arg Gln Ala Tyr His Ile Arg 120 125 Tyr Lys Lys Ser Leu Glu Glu Asp Val Ala Ala His Thr Ser Gly Asn 130 135 Phe Arg Lys Leu Leu Val Ala Leu Val Ser Ser Tyr Arg Tyr Glu Gly 150 155 Pro Glu Val Asp Met His Leu Ala Ser Tyr Glu Ala Lys Lys Leu Ser 165 170 Glu Ser Ile Thr Glu Gln Lys Arg 180

<210> 119

<211> 568

<212> DNA

<213> Eucalyptus grandis

## <400> 119

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                                                                        60
ggttctacgt ccaggacggc aaagtaattc caaactctat ggtaaacctc tccggtcttc
                                                                       120
ccaaagtcaa ctcgatcacg tcagattact gcaccgctaa aatggacgtt ctcgacgatt
                                                                       180
ctaccgcttt caacgtacat ggtggtcttg caaagatggg taaatccctt gcacgaggag
                                                                       240
cagtactcgt ggtcagtctc tgggatgatc ttggcggcgg gatgacttgg ttggatggtc
                                                                       300
tagcagggga tgcatctgcc cctgggaccc tccgtggacc gtgcaccgct gcgaatgtaa
                                                                       360
catcagatcc ggctacctcc gtcactttct cgaatatccg agttggcgat atcaatagca
                                                                       420
ctttctctca ggtgcacttt gggcaatgtg gaggtcaatt ttacgagggg ccagctcttt
                                                                       480
gcgcagaccc attcgagtgt gtcttcagta atccgtatta cagccagtgt ctataagata
                                                                       540
ttgaatataa cacggtttat gtccttcc
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<210> 120

<211> 360

<212> DNA

<213> Eucalyptus grandis

<400> 120

<211> 619

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gcaggtcggt acccagactg ctgaatctca tccgcctctt acctggcaaa aatgtacgac
                                                                      120
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Tyr Cys Thr Ala Lys Met Asp Val Leu Asp Asp Ser Thr Ala Phe Asn
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Val His Gly Gly Leu Ala Lys Met Gly Lys Ser Leu Ala Arg Gly Ala
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Val Leu Val Val Ser Leu Trp Asp Asp Leu Gly Gly Met Thr Trp
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Leu Asp Gly Leu Ala Gly Asp Ala Ser Ala Pro Gly Thr Leu Arg Gly
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Pro Cys Thr Ala Ala Asn Val Thr Ser Asp Pro Ala Thr Ser Val Thr
                            120
                                                 125
Phe Ser Asn Ile Arg Val Gly Asp Ile Asn Ser Thr Phe Ser Gln Val
                        135
                                             140
His Phe Gly Gln Cys Gly Gln Phe Tyr Glu Gly Pro Ala Leu Cys
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Ala Asp Pro Phe Glu Cys Val Phe Ser Asn Pro Tyr Tyr Ser Gln Cys
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Leu
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Gly Ser Val Val Ile Asp Ala Asn Trp Arg Trp Val His Ser Ile Asn
Gly Thr Thr Asn Cys Tyr Thr Gly Gln Ala Trp Asn Thr Thr Leu Cys
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Pro Asp Asp Thr Thr Cys Ala Ala Asn Cys Ala Leu Asp Gly Ala Asp
Tyr Ser Gly Thr Tyr Gly Ile Thr Thr Ser Gly Asn Ala Leu Thr Leu
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Lys Phe Val Thr Gln Ser
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Phe Ser Phe Trp Val Leu Ala His Leu Tyr Pro Phe Ala Lys Gly Leu
Met Gly Arg Arg Gly Arg Thr Pro Thr Ile Val Phe Val Trp Ser Gly
Leu Ile Ala Ile Thr Ile Ser Leu Leu Trp Val Ala Ile Ser Pro Pro
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Asp Ile Leu Thr Gly Phe Lys Met His Cys His Gly Trp Arg Ser Val
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Tyr Cys Ile Pro Lys Arg Pro Ala Phe Lys Gly Ser Ala Pro Ile Asn
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                                        75
Leu Ser Asp Arg Leu His Gln Val Leu Arg Trp Ala Leu Gly Ser Val
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Glu Ile Phe Leu Ser Arg His Cys Pro Ile Trp Tyr Gly Tyr Gly Gly
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Gly Leu Lys Trp Leu Glu Arg Phe Ser Tyr Ile Asn Ser Val Val Tyr
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Pro Trp Thr Ser Ile Pro Leu Ile Val Tyr Cys Ser Leu Pro Ala Ile
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135

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Cys Leu Leu Thr Gly Gln Phe Ile Val Pro Glu Ile Ser Asn Tyr Ala
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Ser Leu Val Phe Met Ala Leu Phe Ile Ser Ile Ala Ala Thr Gly Ile
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Leu Glu Met Gln Trp Gly Gly Val Gly Ile Asp Asp Trp Trp Arg Asn
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Glu Gln Phe Trp
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Leu Leu Asp Ala Ser Thr Val Ala Glu Ala Ile Ser Ala Ile Ser Cys
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Trp Tyr Glu Asp Lys Thr Glu Trp Gly Glu Arg Val Gly Trp Ile Tyr
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Gly Ser Val Thr Glu Asp Val Val Thr Gly Tyr Arg Met His Asn Arg
Gly Trp Thr Ser Val Tyr Cys Val Thr Lys Arg Asp Ala Phe Arg Gly
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                                105
Thr Ala Pro Ile Asn Leu Thr Asp Arg Leu His Gln Val Leu Arg Trp
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Ala Thr Gly Ser Val Glu Ile Phe Phe Ser Arg Asn Asn Ala Ile Met
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Ala Ser Gly Arg Leu Lys Phe Leu Gln Arg Ile Ala Tyr Leu Asn Val
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Gly Ile Tyr Pro Phe Thr Ser Ile Phe Leu Ile Val Tyr Cys Phe Leu
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Pro Ala Leu Ser Leu Phe Ser Gly Lys Phe Ile Val Gln Ser Leu Ser
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Val Ser Phe Leu
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Gly Met Glu Gly Tyr Asp Asp Glu Arg Ser Leu Leu Met Ser Gln Lys
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Ser Leu Glu Lys Arg Phe Gly Gln Ser Pro Val Phe Ile Ala Ala Thr
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Phe Met Glu Gln Gly Gly Leu Pro Pro Ser Thr Asn Pro Ala Thr Leu

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Ile Leu Thr Gly Phe Lys Met His Ala Arg Gly Trp Ile Ser Ile Tyr
                            120
Cys Met Pro Pro Arg Pro Ala Phe Lys Gly Ser Ala Pro Ile Asn Leu
                        135
Ser Asp Arg Leu Asn Gln Val Leu Arg Trp Ala Leu Gly Ser Ile Glu
                   150
                                        155
Ile Leu Leu Ser Arg His Cys Pro Ile Trp Tyr Gly Tyr Asn Gly Arg
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Leu Lys Trp Leu Glu Arg Leu Ala Tyr Ile Asn Thr Ile Val Tyr Pro
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Thr Trp Lys Lys Cys Ser Ser Gly Gly Ser Cys Thr Ser Val Asn Gly
Glu Val Thr Ile Asp Ala Asn Trp Arg Trp Leu His Gly Thr Ser Asp
Thr Lys Asn Cys Tyr Asp Gly Asn Lys Trp Thr Asp Lys Cys Ser Ser
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Ala Thr Asp Cys Ala Ser Lys Cys Ala Ile Glu Gly Ala Thr Tyr Ser
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Lys Thr Tyr Gly Ala Ser Thr Ser Gly Asp Ala Leu Thr Leu Lys Phe
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Met Asn Ile Val Trp Arg Leu Leu Ala Gly Ser Pro Met Pro Ser Ile
Met Gly Met Ile Arg Gly Val Pro Ser Leu Val Gly Tyr Phe Ser Pro
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705			Tyr		710					715					720
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<212> PRT

<213> Eucalyptus grandis

<400> 146

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tcaaaccgca gtccagaacg ccaatctgca gagctccata aaggtctcca ctacccacgc
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cacgtctgtt ctgggaaact cgtatccccc ttctcaggga gaattcgctg atgaattgaa
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gagtagcatg agcgatgtac ttaactttct ggcagagaat gggtctcctt tcatggctaa
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cgtgtatccc tacttcagtt acatttacaa ccaggcccaa atctcgttag actatgcttt
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gtttaaatcc gcggatcccg tggtgagtga tgaaggtcgt ctctataaaa gcttgttcga
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                                                                       240
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      <212> DNA
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ccgtctaaag gagtcttcgt agatgctgtg aaagacacga tgagccaaat actcaatttt
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ctgtcacaga acggtggtcc cttcatggcg gacgtctatc catacttcag ctacatcggc
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aacacaaaag acatttctct ggattatgct ctgtttaagt ctacgtctac ggtggtgcaa
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gacggtgatc acagctacac caacctgttc gatgccatgg gtgatactct t
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aatagtgggt gtcgctaacg aagaactgaa gaacatatct tccagccaag actcggcaaa
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ccgttgggtt aacgagcaca ttgtgccctt ctatcccgcc accaatgtca aatacattgc
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ggccatgaac aacattcaaa ctgcgatcca gaacgctaaa ctgcagaata qcatcaaqqt
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ctctaccacc cacaggccgg atgttagcag cggcaacctg ccgtctgaag gagtcttcat
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aggacatato ttocagocaa gactoggoaa acogttgggt taacgagaac attgtgcoct
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totatocogo caccaatgto aaatacattg cagtgggaaa cgaagttttg ataggcaacg
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ttcagtacgt accetatett gttccggcca tgaagaacat tcaaactgcg atccagaacg
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gtcacagaac ggtggtccct tcatggcgga cgtctatcca tacttcagct acatcggcaa
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cacaaaagac atttctctgg attatgctct gtttaagtct acgtctacgg tggtgcaaga
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cggtgatcac agctacacca acctgttcga tgccatggtt gatactct
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gaggacatat cttccagcca agactcggca aaccgttggg ttaacgagaa cattgtgccc
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gttcagtacg taccctatct tgttccggcc atgaagaaca ttcaaactgc gatccagaac
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gctaaactgc aggatagcat caaggtctct accacccaca ggccggatgt tagcagcggc
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tacccgccgt ctaaaggagt cttcgtagat gctgtgaaag acacgatgag ccaaatactc
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aattttctgt cacagaacgg tggtcccttc atggcggacg tctatccata cttcagctac
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atcggcaaca caaaagacat ttctctggat tatgctctgt ttaagtctac gtctacgggg
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tgcaagacgg tgatcacagc tacaccaacc tgttcgatgc catggttgat actc
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ggtccattcc atcaacggta ctactaactg ttacactggt caagcatgga acacgacact
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ctgtccggat gacacgactt gcgcagccaa ctgcgctttg gatggtgctg attactctgg
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cacttatggc attactactt ccggcaatgc tcttaccctc aagttcgtca ctcaatcttc
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ctttggccat tgttccatta catgttgcct ttgtcgcctg acctcggtgg tcggttcaac
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cggtccttgt ggcaggctta tgtctccgtc aataagattt tcgcagatag gatcatggaa
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actttcttga ggaaaaggtt caatagagtg aagcttggct tcttccttca cagcccattc
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      <400> 188
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caatgaacac tgtatttatt atcagtgggc gggggagaaa atcattaagt gagtggcttt
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cttcttgcaa gaagcttgga atagccgctg agcatgggta ttttataagg tggaacagtg
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cagccgagtg ggaaaccagt tcattgtctg ctgatcttga ttggaagaat accgtggaac
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tgttggctca tctagagagt gtgctcgcaa atgaacctgc agttgttaag aggggacagc
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ccgcccaaca gcgcatgaga aatagttttc ccccttgaga tcgagcacat tccaagatat
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tttatccgga gatgacctcc tcccactacc actggcatgg ttgttagttc ttttctcaqq
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gtttggtaaa ggtcgttgtg tcttcaccgc agacgctttt gacccgcttt tactagcttg
                                                                       300
aagcttcaat gaagatcgtt tctcccctg
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tocatoagtg tgatacotac tgctgagaca gttggactca ttaacagttt gtgccgagat
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cccaagaatg ttgtcttcct tgtcagtgga aaggagcgag ttatcctaag taaatggttc
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tcatcgtgtg atagacttgg gttagcagca gagcatggct attttcttag gccaaaccaa
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gaaggagatt gggaaacttg tgtttcggtg acagattttg actggaaaca gacagctgag
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ccggttatga gattatacat ggaaacaact gatggctcta ctatagaaat caaagagagt
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tcaattgtgt ggaactacca gtgcgcagat ccagattttg gtttttgcca ggcaaaggaa
                                                                       420
cttttagatc acctggaaag tgttcttgca aatgaacctg tttctgtcaa gagtggccaa
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cacattgtgg aagttaaacc tca
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tcatcaaget gaggatgggg ttetttetee atagecettt tecatcatea gagatatata
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ggactettee agnnagggag gagatactea aagegettet taatgetgae etgattggtt
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tccacacgtt cgattatgct cggcattttc tatcctgttg cagtagaatc tggggngtgg
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agtaccagtc gaaaaggggt tatatcggnt tggaatatta tggaagaaca attggggtaa
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agatttacaa gactctgccg atcanggagg agcttctgan ggctttcctg aattctgatt
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tgatagggtt ccacactttc gactatgcac gccatttcct gtcttgttgt agtcggatgc
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tggcttcttc cttcacagcc cattcccctc ttcagagatt tacaagactc tgccgatcag
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ggggttatat aggcctggac tattatggtc ggactgttag tatcaaaatt cttccagttg
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ctgaattctg atttgatagg gttccacact ttcgactatg cacgccattt cctgtcttgt
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tgtagtcgga tgcttggtct tacctatgaa tcgaagaggg gttatatagg cctggactat
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tatggtcgga ctgttagtat caaaattctt ccagttggga tacacatggg acaattgcag
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attttggcga actcgacatg tggttagcag cagaaaatgg tatgtttctg cgccatacga
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aaggagaatg gatgatcaca atgccagaat atcttaatat ggactggatg qaqaqtqtaa
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agettgtttt tgattatttc aaagaaagge acetegateg tatgtngagg ttegagaaac
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agagaccett catattgtcg cgctcgacgt acgtgggctc cgggaagtat gtngctcact
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ggaccggaga taaccaaggn aattgggaaa atctgaagta ttccatctcc actatgctga
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cactacaacg gcgtcctcga g
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      <212> DNA
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ccccacaaac cggagctgcc cgggcacggt ttcccatggg actgctgcct cgactgcaca
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caacttgage tgctgaacgt cactgeegta gateceacag gtageggega gagteaggte
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agcg
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gacttcaccc ttgaccctat caactatcct gaatataagc tgcgtccctt ccttgaccga
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ccgttcttgg gtcaggtgtg gcccggcgcc gtgtactttc cggacttcct gaacccaaag
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      <213> Pinus radiata
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gacttcaccc ttgaccctat caactatcct gaatataagc tgcgtccctt ccttgaccga
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ccgttcttgg gtcaggtgtg gcccggcgcc gtgtactttc cggacttcct gaacccaaag
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gaggccaacc gccaggccta caggacactc ctggtcagtg ctccggggct tggccagtac
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ggccggaaca gcaggaggca ctgttcgctg cagggcacga acggtgtact cagcaatgac
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ct
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				gagaaggaaa		300
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tggcacagaa	caatgtgttg	tttgagggta	ttttqttaaa	gccaagtatg	gtgactcctg	300
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acaatggtot tgtgcccatt gtggagcnag agattcttct ggatggagac cattgcattg
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acagaagcct tgaagtggcg gagaaagtct gggctgaggt tttcttttac ttggcacaga
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gcaacattga atttgaatgn aatgaaccaa agcccaaacc catggcatgt ttccttttca
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tcctggggtt atgttcttgt ctggaggaca gtctgaggtt gaggcaactt tgaatttgaa
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tgcaatgaac caaagcccaa atccatggca tgtttccttt tcatatgcac gtgccttgca
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gaatacatet eteaagaeet ggaagggtet teeagagaat gttgaageag eteagaggge
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gettettatt egggecaagg ctaattetet ggeceagett gggegataet etgetgaagg
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557

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gaaattacta ttggccttgg tccgtcaggt gaactaaggt accctgccca tccttttct
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      <400> 258
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tattttagtc atatagttgc cctttttatt tactagtttg gatttccttg tattgcagta
                                                                       180
tatgatetet aacettagat eeacgteega agetgetgga aageaggagt ggggtaatgg
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agatggtggc tggaacagtt cttatggtga gttttttctt gagtggtatt ctcgtatgct
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      <212> DNA
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agatgtttgg tagtgaacag ccagagatat gctgctgcag tccggagggt ctcattaggc
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agatgagaga agttgcaagg cgaggaaata tacctttaac aggtgaaaat gcaattgaac
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gctttgataa ggaggctttc tctcaaattg tgagaaatgc ttacaatcgt cctcaggatg
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tgagagcctt tacgtatttc cgaatgaggg aggcactgtt caggactgat aattggaaat
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gccttaaagg ctcttggtgt ggatggagtg gttatgcaag tattttgggg cattgtggag
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agagatgete caacaaaata tgactggtet geatatttgg etttggtgaa aatggtecaa
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gcagcaggcc tgaaagttca ggcttcaata tgctttaatg gttgtaaatc tagtcaagaa
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agettgteta tacetettee atettgggtt ettacagtgg geaatagtga tecagacate
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      <212> DNA
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acatgaggag tttcaaggag aattttgggg atcttctggg agaaaccatt gtggaaattc
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aagtgggaat gggtcctgca ggagagctga ggtatccatc ttatcctgag agtaatggta
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cctggagatt cccaggaatt ggagcatttc agtgctatga taagtatatg gtctctaacc
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      <212> DNA
      <213> Pinus radiata
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ggctcttgtg cgtcaggtat taaatgctgg atggaaagaa ggtattgagg tttcctgtga
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cgagggaata aacgaaacag gaccgcccaa gaagcgaata tctgctttta cctatctaag
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gctatctcaa gaactcatgc aagaacatag ctggaaagaa ttcaacaaat tcctgagaag
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aatgcatgtg agtttggatt atcat
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      <212> DNA
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tgccagtggg gtgacggctc cgagcccatc ggtaactggg cccccatgaa cctgggtgtt
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ggctactctg ccggctccac ctggttgtcc atgttcaaga acgagcctac cacctctgcc
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aacctggact tcaagatcaa gattatcggt gacgacctga gcgacaactg cagctacgac
                                                                       240
ggagccggca acttctacaa caaggccggc ctgatcacct ctggcaacgg ctgcactgtc
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ageteeteet etggeaacge etaettegte
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105

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aatttgatca ggctatgcag catgttgaag aagcttatgg cttcatgact tctgagcacc
                                                                     180
aatacatatc cagaaaagat gaaggagaca gggtcatcgt ctttgaaagg ggaaatcttg
                                                                  .. 240
tgtttgtctt caatttccat tggaataata gctacacgga ctaccatgta ggctgcttga
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agcctggaaa gntaagattg tcttaaattc agatgacgcc ttgtttggag ggtatagta
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      <212> DNA
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gagttgagct tgaagatcgg ccaaaagttg tccctccacc tgggagtggc caaaggattt
                                                                     180
atgaaataga tocattgttg aataactato gtgaacatot tgattatoga tttgcgcagt
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ataagaaaac aagagagttg attgataaat atgaaggtgg cttggaagca ttttctaggg
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gttatgaaaa gatgggattt aatagaagtg cggctggaat cacatacaga gagtgggcac
                                                                     360
ctggtgctaa gggggcatca cttataggag atttcaacaa ctggaatccc aatgctgatg
                                                                     420
ttatgctaag aacgagtttg gagtatggga g
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ttaagataca tatggataca atttcgggac caaaggacgc aatccctgct tggattaagt
                                                                     180
ttgctgttca agctccgggt gagattccat acaatggaat atattatgat cccctcctg
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aggataaata tgaatttaag tatcctcgac caaagcagcc caaatcattg cgaatatatg
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aagcgcatgt tggcatgagc agcacggaac ccaaaattaa tacatatgtt gagttcaggg
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atgatgtact accac
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      <211> 408
      <212> DNA
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acaagatgat tcatttcata acaatggcac taggtggcga gggctatctt aattttatgg
                                                                     120
gaaatgagtt tggtcatccg gaatggattg actttccaag ggaaggaaat ggttggagct
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atgaaaaatg tagaagacag tggaacttag tggacacaga tcacctgaga tacaagttta
                                                                     240
300
caaagcaaat agttagcatt gcaaatgaag aagataaggt gattgttttt gaacgaggcg
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atatagtgtt tgttttcaac ttccatccca agaatacata tcctgggt
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     <211> 476
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ttggttatca ggtcaccagc tttttcgctg ccagctctcg atatggtact cctgaggagc
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tcaaggagct gatcgatacc gcgcattcaa tgggcatcac tgtattgctt gatgtagtac
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agtacttcca tggaggacca aagggatacc acgacttgtg ggacagtcgt ctcttcaact
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actotoatta tgaggttoto cgottootga tgtotaatot gogottotgg atggaagagt
                                                                        420
atcagtttga cggtttccgc tttgatggtg ttacgagtat gttgtatctg catcac
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      <211> 313
      <212> DNA
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gtctaccacg aatgggcccc gaacgccgta gaggcctccc taatcggaga tttcaacaac
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tgggaccgac actctcatgc tatgaccaaa gatcagtatg gtgtctgggg aatcacgatc
                                                                       180
cctagcatca acggacagcc tgctatcccc cacgattcga aaataaaggt ttcgttcgtt
                                                                       240
attectggeg gegagegtat egagegtetg cetgettgga teaagegegt cacceaggae
                                                                       300
ctctctgtct cgc
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      <211> 258
      <212> DNA
      <213> Pinus radiata
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gtactttgga tttgctactg atgtagatgc tgtggtttat ttgatgctgg ttaatgacat
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gattcatggt ctatttcccc aggccataac aattggagaa gatgtgagtg gtatgccaac
                                                                       180
cttttctcgt tctgtacaag atggcggagt gggatttgat tatcgactcc atatggcagt
                                                                       240
agctgacaaa tggattga
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      <210> 271
      <211> 349
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      <213> Pinus radiata
      <400> 271
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gatcggccaa aagttgtccc tccacctggg agtggccaaa ggatttatga aatagatcca
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ttgttgaata actatcgtga acatcttgat tatcgatttg cgcagtataa gaaaacaaga
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gagttgattg ataaatatga aggtggcttg gaagcatttt ctaggggtta tgaaaagatg
                                                                       240
ggatttaata gaagtgcggc tggaatcaca tacagagagt gggcacctgg tgctaagggg
                                                                       300
gcatcactta taggagattt caacaactgg aatccaatgc tgatgttat
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      <210> 272
      <211> 369
      <212> DNA
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      <400> 272
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cctttcttgt gtatgcacct tgcagaactt cagttgtcta tagtcttaca gatgattaaa
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tgagaataaa aataagatgt ttgccttgta tccaaatttt accggaaggg aatacatgat
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cgcaacatgt ttgtatgact gaagaaagca gtatttctaa aacagatatc ggaggacatg
                                                                        300
gcttctccca ttatcttgtt tttccatata aatctcactt gggcatacca tctttagttc
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tgtagtcag
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      <210> 273
      <211> 327
      <212> DNA
      <213> Eucalyptus grandis
      <400> 273
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accetecace tecaceegeg atecegatgg ettecegeaa caatggcate teeggeggea
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agggcctcat cgtgagcttc ggcgagatgc tcatcgactt cgtcccgacc gtgtcggggg
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tetecetgge ggaggeeceg gggtteetea aggeeceegg eggegeecee gecaacgteg
                                                                       240
cgatcgccgt gacccgcctc ggcggccggt ccgcgttcgt cggcaaagct cggggacgac
                                                                       300
gagttcgggc aacaatgctg gccggat
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gcattagctt ttgttaccaa tagagctgat ggggagcgag agttcctatt ttttcgtcat
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ccaagtgcgg ccatgctttt acatgaatcg gaaactagat gttgaactta tcagcaaggc
                                                                       180
aaagatette cattatggtt etateagttt gattgatgaa eeetgeaaat eggeteatet
                                                                       240
tgcagcaatg aaaattgcca aaaactcagg gagcg
                                                                       275
      <210> 275
      <211> 362
      <212> DNA
      <213> Eucalyptus grandis
      <400> 275
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acttcgtccc gaccgtgtcg ggggtctccc tggcggaggc cccggggttc ctccaacgcc
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cccggcggcg cccccgcaac gtcgcgatcg ccgtgacccg cctcggcggc cggtccgagt
                                                                       180
tegteggeaa gateggggae gaegagtteg ggeacatget ggeegggate etaaaegaea
                                                                       240
acggggtcaa ctgcgacggc atcaacttcg accagggggc gcggaccgcg ctggccttcg
                                                                       300
taacgctccg tgccgacggg gagcgcgagt tcatgttcta ccggaacccg agcgccgaca
                                                                       360
tg
                                                                       362
      <210> 276
      <211> 543
      <212> DNA
      <213> Eucalyptus grandis
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aaaggagtet gtgacaccat acgcagggga gcaatgggaa tacagaagca gcaggaatgc
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taaccagact ctcttcaatt gaaaatggaa gcaagcaacg actagtccta agggaaaatc
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agagaatgga agaattggag cttgttcgaa tgctttattt cgtgccatcg atcaagctga
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ggacatcage cteggteggg agggegggga tegeteeett ettggtggtg gtgatggete
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ggtcgtcaan aatgttgcag aggagtgccc cgacaaagga atcaccagcc ccggttgtgt
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caaccgtgtt aacatggaat gcttcnacat gtccatgaaa atgcttggtg tagtatctac
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aaccgtgctc acccaaagta acaaggagaa gtgtcaagtt ggggtgccac agtgtcattg
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cat
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gggagtgaca agattgatga tgaaaatgca atgacactgt ggcaccccaa cttgacactt
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ctccttgtta ctttgggtga gcacggttgt agatactaca cca
                                                                       163
      <210> 278
      <211> 270
      <212> DNA
      <213> Eucalyptus grandis
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                                                                       120
egegtgegga neateaceae caccaagaag ggagegatee eegeeeteee gaeegagget
                                                                       180
gatgtcctca gcttgatcga tggcacgaaa taaagcattc gaacaagctc caattcttcc
                                                                       240
attctctgat tttcccttag gactagtcgt
                                                                       270
      <210> 279
      <211> 201
      <212> DNA
      <213> Eucalyptus grandis
      <400> 279
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ttgacgaccg ctccattctc gaagatgaag gaaaattgag gaaagtcctg aagtttgcaa
                                                                       120
acgcgtgcgg agccatcacc accaccaaga agggagcgat ccccgccctc ccgaccgagg
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ctgatgtcct cagcttgatt q
                                                                       201
      <210> 280
      <211> 319
      <212> DNA
      <213> Eucalyptus grandis
      <400> 280
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                                                                        60
agcccgagga gctcaacctc gagctgatca gatctgcgaa agtctttcat tatggatcca
                                                                       120
tcagtttgat tgtggagcca tgcagatccg cccatcttga agcaatgcaa gttgccaagg
                                                                       180
acgctggggc tctgctctcc tatgatccaa acctcagact accattgtgg ccatcacctg
                                                                       240
aggaggeteg tgageagate aagageattt ggggaeaaag geagatatea tttaaaagtg
                                                                       300
gagtgattgt tgaactgga
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      <210> 281
      <211> 446
      <212> DNA
      <213> Eucalyptus grandis
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ceggggttee teaaggeeee eggeggegee ceegeeaaeg tegegatege egtgaeeege
                                                                       180
cteggeggee ggteegegtt egteggeaag eteggggaeg aegagttegg geacatgetg
                                                                       240
gccgggatcc tgaaggagaa cggggtcaac tgcgacggca tcaacttcga ccagggggcg
                                                                       300
cgtgaccgcg ctggccttcg tcacgctccg cgccgacggg gagcgcgagt tcatgttcta
                                                                       360
ccggaacccg agcgccgaca tgctgctcaa gcccgaggag ctcaacctcg agctgattan
                                                                       420
gatctgcgaa agtctttcat tatgga
                                                                       446
      <210> 282
      <211> 369
      <212> DNA
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      <400> 282
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ctcaageceg aggageteaa eetegggget gateagatet gegaaagtet ttcattatgg
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atccatcagt ttgattgtgg agccatgcag atccgcccat cttgaagcaa tgcaagttgc
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caaggacgct ggggctctgc tctcctatga tttaaacctc agactaccat tgtggccatc
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acctgaggag gctcgtgagc agatcaagag catttgggac aaggcagata tcattaaagt
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gagtgatgt
                                                                       369
      <210> 283
      <211> 583
      <212> DNA
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getteggega gatgeteatt gaettegtee egacegtgte gggggtetee etggeggagg
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ccccggggtt cctcaaggcc cccggcggcg ccccgccaa cgtcgcgatc gccgtgaccc
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ggettggegg ceggteegeg ttegteggea tgetegggga egaegagtte gggeaeatge
                                                                       240
tggccgggat cctgaaggag aacggggtca actgcgacgg catcaacttc gaccaggggg
                                                                       300
egeggacege getggeette gteaegetee gegeegaegg ggagegegag tteatgttet
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accggaaccc gagcgccgac atgctgctca agcccgagga gctcaacctc gagctgatca
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gatctgcgaa agtctttcat tatggatcca tcagtttgat tgtggagcca tgcagatccg
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ccatcttgaa gcaatgcaag ttgccaagga cgctggggct ctgctctcct atgatccaaa
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cctcagacta ccattgtggg catcacctga ggaggcttcg tga
                                                                       583
      <210> 284
      <211> 305
      <212> DNA
      <213> Eucalyptus grandis
      <400> 284
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teeggeggea agggeeteat egtgagette ggegagatge teattgaett egteeegaee
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gtgtcggggg tetecetgge ggaggeeeeg gggtteetea aggeeeeegg eggegeeee
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gccaacgtcg cgatcgccgt gacccgcctc ggcggccggt ccgcgttcgt cggcaagctc
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ggggacgacg agttcgggca catgctggcc gggatcctga aaggagaacg gggtcaactg
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cgacg
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      <210> 285
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<211> 403

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      <400> 285
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ttegaaceet ceaceegega teeegatgge tteeegeaac aatggeatet eeggeggeaa
                                                                       120
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gaactgcttt ggcttttgtc acattgaaag ccgatggtga acgagagttt atgtttttcc
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ggaatcccag tgctgatatg ctactaactg aatctgagct tgacgtggac ttaatccaac
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aggctaaaat tttccattat ggatcaatta
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cgtcgcatcg ggccgcctcg cgaaggttaa tcgatcggct tcgttgtcgc tcactattcg
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gcaacggagg tctcaaggtt ctgcaagagc atcagtagca gacaacaaag agcagctgac
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aggtgaatca ccacttgtgg tttgctttgg agaaatgctg attgatttcg tcccaacagt
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tgccggattg tcattatctg aagcgcaggc cttcaaaaag gctcctggag gtgcacctgc
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gggtatttta agcatatggg ataaagcaga tttaattaag gttagtgaag aggaagtagg
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ttttagcgga agagtgaaag gcctggcagt ggaagctgta gacaccactg gtgctggaga
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gtttgggcgc atgcttgctg acattctgag ggaaaacaat gtgatggacc gaggaattag
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atttgattcc catgccagaa ccgcgctggc attcgttact ttaaagatga atggcgagag
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ggaatttatg ttctatcgta atcccagegc tgacatgctt ctcaaggaat ctgagcttga
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tgcaaagctg atcccagagg catcgatatt tcattatgga tcaatcagtc tgattgcaga
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accttttcca tccaaacctc aaattgcttc tcgtgactga aggccagcaa ggatgtagat
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attacaccaa ggattttagc ggaagagtga aaggcctggc agtggaagct gtaaacacca
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tattcagcga gggtgtggtg aagcgcgagg atttgtggat cacatccaag ctatggtgtg
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gccatcaagg ttgggtacag gcatattgat tgtgctcaag cttatcaaaa tgagaaggag
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ggtgaagcgc gaggatttgt ggatcacatc caagctatgg tgtgctgatc acgcaccaga
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ttacctgatc cactggccgg tgagcatgag gaaggctcaa tttggcttca agcctgaaaa
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tetetaettt eggeeegtge tgegggtgea gageetattg ttataaegga eett
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tetttegaag agggegeett gtgegaacea etegetgteg cattggeegg categagegt
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agccgtctgg actttgcgaa gaagctggtg cctggcgttc qcac
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teeggtetea gaeteggaga teeegtéett gtetgtggtg etggaceaat aggeetaate
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tcaagcttat caaaatgaga aggagattgg tactgctctc cagaaattat tcagcgaggg
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tccagaaatt attcagcgag ggtgtggtga agcgcgagga tttgtggatc acatccaagc
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tatggtgtgc tgatcacgca ccagaagatg ttcccaaggc attagaaaga accctggaga
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agateceete categggetg ggeacttgge aggeegatee eggegtegtg geegaggeeg
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agaaggagat tggtactgct ctccagaaat tattcagcga gggtgtggtg aagcgcgagg
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atttgtggat cacttccaag ctatggtgta ctgatcacgc accggaagat gttcccaagg
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PCT/NZ99/00169

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cgtgttggcg ttgtgaccaa tgtaagcgag gctcctacaa tttgtgtccc gagatgaagt
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180

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gaacgtggag gtgggtaaaa cgaagactaa tatcatgttg attggagaag gcatggaggc
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catgaatete ettgtatgaa tteteeaaca gtaaaettge tegeetettg agaaettgtg
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attacccgat acccggccca tttcacgcgg ttagcagttg ctgctcctgg gcctgtattc
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gcaggctgaa taacatcgtc tagata
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agactaatat catgttgatt ggagaaggca tggaggccac aatcgttaca gggagcagaa
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tgtgatagac ggatcnccac tttcaattca gccacattcg ctgctgtagg gaagggattt
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atggcacaag acatggcgtt cgtcaacaca gcaggcccgg acaaacatca ggcggtggct
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atgtattete cataatacaa agtttgcaat gcaaaactte cattecatte cagecagece
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gcaggctgaa taacatcgtc tagataggac tgcatgtaaa ccgttcggga atactccttc
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cacggeetee ccagatatgt tgggaatgag ettttcaccg gaacaaggte ggeateggga
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gtgatcttgc agttgtga
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tgatcccaca cgcagggcca ccgcctggtg cttcgcgggt cctgccgtgt tctcgaaggt
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gaaattgtcc ttcacatttc ggtttccggt caccactgtg acatccatac catctccaac
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gaacatgata ttaagttttc ttcttgtgca actccacatt ctctgcataa actcctgctt
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tatatgaata cgtatctcgt
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catgtcgcga gcgatgaatc catttccagt cacagcaaca gttgcagaac gaaaggttgt
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gaaattgtcc ttcacatttc ggtttccggt caccactgtg acatccatac catctccaac
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gaacatgata ttagttttct tcttgtgcaa ctccacattc tctgcataaa ctcctgcttt
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tatatgaatt acgtatctcg tctggctctt ctccggagcc ttctccactg cctctgtaat
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gttcgtgtaa tttccactg
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      <212> DNA
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canaacacag ccccggttcc tctgccgggg gcggtgggca gacaagcagt ggccttgaga
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tatgaccacg ctggccgcca ttatttcaaa gactgttata tcgaaggctc cgtcgatttc
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atcttcggga acggcctctc cctctacgag gggtgcagcc tgcatgggat ttccgatacc
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gggtttacgg ggaaacggtt cgaatccccc gcagtaagac gaatctcgtg tttgtgggcg
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ccggtatgga taaaacggtg atcaccggtt ctgcatatgt gccgtctctg cccggcccgc
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tcacaattta cgatgtcgcc acggttggag tgaatgggga cggcttcata gcccgtgaca
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taacattccg aaacacattt caggggccac agactcatca agccgtggcc ctgagagtag
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acagegattt ttetgeette tacagetgeg etttegagag ceaceaggae acgetetaca
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cgcacacgct ccgccaattc tacagaaatt gcagaataga gggcacccac gacttcatct
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      <212> DNA
      <213> Pinus radiata
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caacaaaaag gcgacgcctt ttggcagagg caggggaaga aatgaacaat gctcttcgga
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ggtggttatc ttcccgagat cgcaggcttt tgaaactgcc cgttgctgcc atgcaacctg
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atgcaccttc cctgctaagc agcagaaggt atatcatcta tgtgaaaaca ggcgtgtata
                                                                       420
acgaaaatgt cacgatttca aggaagaaga ccaatctcat gattgttggt gatggcattg
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gaaaaactat tgtagcagca ggcaa
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ggctctggaa aattcaaaac aattacagaa gccatagctg cggccccgga gaaaagctct
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aagagatacg tgatcaaggt gaagaagggg acgtacaagg agaacgtgga agtgggcaaa
                                                                       180
aagaagacaa atattatget gategganaa ggeatggaag ceaegategt tacagggage
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agaaatgttg tagacggttc caccactttc aatteeteta cactagetge tgtagggaag
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gggtttatgg cacaagacat ggcgttcgtc aacaccgcag gtccagataa gcatcaagcg
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caggagateg gaggeteeta egeteettte caaacgacat egtggetgae gtgategtgg
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ctcaggatgg ctctggaaaa ttcaaaacaa ttacagaagc catagctgcg gccccggaga
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aaagctctaa gagatacgtg atcaaggtga agaaggggac gtacaaggag aacgtggaag
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tgggcaaaaa gaagacaaat attatgctga tcggagaagg catggaagcc acgatcgtta
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tagggaaggg gtttatggca caagacatgg cgttcgtcaa ca
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ccggtatgga taaaacggtg atcaccggtt ctgcatatgt gccgtctctg cccggcccgc
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tcacaattta cgatgtcgcc acggttggag tgaatgggga cggcttcata gcccgtgaca
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taacattccg aaacacattt caggggccac agactcatca agccgtggcc ctgagagtag
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      <213> Pinus radiata
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tategntgea getteaaggg ttaccaggae accetatacg eccatteect tegteagttt
                                                                       120
tacagagaat gcaacatcta tggcaccgta natttcatct tcggcaactc cgccgtcgtt
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tttcaggatt gcaatttgct ggcgcggaga cccctggaga atcagaagat tctttacacc
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gctcacggca ggcaggaccc caatgagaac actggaattt ccattcagaa ctgtaatgtg
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accgcagccc cagacctggc tccagtgaag agctcgttcg atgcatatc
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      <211> 375
      <212> DNA
      <213> Pinus radiata
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ggctctggaa aattcaaaac aattacagaa gccatagctg cggccccgga gaaaagctct
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aagagatacg tgatcaaggt gaagaagggg acgtacaagg agaacgtgga agtgggcaaa
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aagaagacaa atattatgct gatcggagaa ggcatggaag ccacgatcgt tacagggagc
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agaaatgttg tagacggttc caccactttc aattcctcta cactagctgc tgtagggaag
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gggtttatgg cacaagacat ggcgttcgtc aacaccgcag gtccagataa gcatcaagcg
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gtggctcttc gtgta
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      <211> 367
      <212> DNA
      <213> Pinus radiata
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aagctgtgaa cagtgcgccg gactactcgg aaaagaaatt tgtgatcaag atacaggccg
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gggtttacgg ggaaacggtt cgaatccccc gcagtaagac gaatctcgtg tttgtgggcg
                                                                       180
ccggtatgga taaaacggtg atcaccggtt ctgcatatgt gccgtctctg cccggcccgc
                                                                       240
tcacaattta cgatgtcgcc acggttggag tgaatgggga cggcttcata gcccgtgaca
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taacattccg aaacacattt caggggccac agactcatca agccgtggcc ctgagagtag
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acagcga
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      <213> Pinus radiata
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ggctctggaa aattcaaaac aattacagaa gccatagctg cggccccgga gaaaagctct
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aagagatacg tgatcaaggt gaagaagggg acgtacaagg agaacgtgga agtgggcaaa
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aagaagacaa atattatgct gatcggagaa ggcatggaag ccacgatcgt tacagggagc
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anaaatgttg tagacggttc caccactttc aattcctcta cactagctgc tgtagggaag
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gggtttatgg cacaagacat ggcgttcgtn aacaccgcag gtccagataa gcatcaagcg
                                                                        360
gtggctcttc gtgtaggatc agaccaatca gtgttatatc gctgcaagat tgcagcgtac
                                                                        420
caagacacat tgtacgcgca ttctct
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      <211> 345
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      <213> Pinus radiata
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aaagcgttgg gtacatataa cagcgctact gttgcagtca attcgcctta cttcatcgcc
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agaaacatta egitteagaa cacagedeeg giteeteige egggggeggi gggeagacaa
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gcagtggcct tgagaatcac gggagacacg tcgtccttct tcgggtgcag cttcttgggc
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gcgcaggaca ctttgtatga ccacgctggc cgccattatt tcaaagactg ttatatcgaa
                                                                        300
ggctccgtcg atttcatctt cgggaacggc ctctccctct acgag
                                                                        345
      <210> 474
      <211> 268
      <212> DNA
      <213> Pinus radiata
      <400> 474
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tgtgaaggac aatttcacaa cctttcgttc.tgcgactgtt gctgtgactg gaaacggatt
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categotege gacatgacet tegagaacae ggeaggacee gegaageace aggeggtgge
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cctgcgtgtg ggatcagatc tctcggcttt ctatcgatgc agcttcaagg gttaccagga
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caccetttac gcccattccc ttcgtcag
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      <210> 475
      <211> 316
      <212> DNA
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acaagaagaa aactaatatc atgttcgttg gagatggtat ggatgtcaca gtggtgaccg
                                                                       120
gaaaccgaaa tgtgaaggac aatttcacaa cctttcgttc tgcgactgtt gctgtgactg
                                                                       180
gaaacggatt catcgctcgc gacatgacct tcgagaacac ggcaggaccc gcgaagcacc
                                                                       240
aggeggtgge cetgegtgtg ggateagate teteggettt etategatge agetteaagg
                                                                       300
gttaccagga caccct
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      <210> 476
      <211> 440
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<212> DNA
      <213> Pinus radiata
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ggagttgcac ccgacgaaaa caaatatcat gttcattgga gatggcatgg atgttacagt
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ggtgaccgga aaccgaaatg tgaaggacaa atttacaacc tatcgttctq caactgttqc
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tgtgactgga aacggattca tcgctcgcga catgaccttc gagaacacgg caggacccac
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gaagcaccag gcggtggccc tgcgtgtggg atcagatctc tcggccttct ataagtgcaa
                                                                       300
cttcaagggt taccaggaca ccctttacgc ccattccttt cgtcagttct acagaaaatg
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caacatctat ggcaccatag atttcatctt cggcaactcc gccgtcgttt ttcaggattg
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caatctcctg gcgcggaggc
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      <212> DNA
      <213> Pinus radiata
      <400> 477
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tgagactgta aatgactggc ctcgcttgag ctattaatca ctcgataccc cgcccatttg
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accegatttg tagtgeeege accagggeeg eggtteatgt attecceata gtacagggtg
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ctgagagcga aggatccatt ccattcgagc caaccggcag gttgaatcag gtcgcccaga
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aaggactgca tgaagacagt gcgagagtac tetttecatg geeteecaag atatgeeteg
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aacgagetet teactggage caggtetggg getgeggtea cattacagtt etgaatg
                                                                       357
      <210> 478
      <211> 318
      <212> DNA
      <213> Pinus radiata
      <400> 478
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taccttggca ggccgtggag aaattactcg cgcactgtgt tcatgaaatc ttatctctac
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gacttgattc agccagcggg ttggttggaa tggaatggca gcttcgctct gagcactctg
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tactacgggg aatacatgaa cagcggcccc ggcgcgggca ctgccaatcg ggtcagatgg
                                                                       240
gcggggtatc aggtgattaa gaaatccaag gaggccaaga aatttacagt gtctcaattc
                                                                       300
attgaaggca attcatgg
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      <210> 479
      <211> 271
      <212> DNA
      <213> Eucalyptus grandis
      <400> 479
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tggaactggc tctgatcata ttcgtgagaa agatgggata tgggctgtgc ttgcttggtt
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atctattctc gcttacaaaa ataaggagaa cttaagtgga gaaaagcttg tatctgtcga
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ngacattgtc cgtcagcatt gggngacata tggtcgtcat tattatacca gatatgatta
                                                                       240
tgagaatgtt gattcaggag cagcaaagga a
                                                                       271
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      <211> 301
      <212> DNA
      <213> Eucalyptus grandis
      <400> 480
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cgtcaganag atgggatatg ggctgtgctt gcctggttat ctattctcgc ttacaaaaat
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aaggagaact taagtggaga aaagcttgta tctgtcgagg acattgtccg tcagcattgg
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gtgacatatg gtcgtcatta ttataccaga tatgattatg agaatgttga ttcaggagca
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gcaaaggaac tgatgggata cttggtccaa ctgcaatcat ctctctctga agtcaaccag
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                                                                        301
      <210> 481
      <211> 287
      <212> DNA
      <213> Eucalyptus grandis
      <400> 481
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tggaactggc tctgatcata ttcgtgagac agatgggata tgggctgtgc ttgcttggtt
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atctattctc gcttacaaaa ataaggagaa cttaagtgga gaaaagcttg tatctgtcga
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ggacattgtc cgtcagcatt gggtgacata tggtcgtcat tattatacca gatatgatta
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tgagaatgtt gattcaggag cagcaaagga actgatggga tacttgg
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      <210> 482
      <211> 285
      <212> DNA
      <213> Eucalyptus grandis
      <400> 482
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tacaagaaca aggaaaatat caatggtgga aagcttgtat cagttgaaga tattgttcgc
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cagcactggg caacttatgg tcgccactat tacactcgtt atgattatga gaatgttgac
                                                                       180
gcaggggcag caaaggaact aatggcatac ttggtccggt tgcaatcttc cctcggtgaa
                                                                       240
gttaatgaga ttgtcaaggg agtatgttcg gatgtgtcaa atgtt
                                                                       285
      <210> 483
      <211> 427
      <212> DNA
      <213> Eucalyptus grandis
      <400> 483
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aaaatggtga cgttccaggt gtcgcgagtg gagaccgcgc ccttcgatgg ccagaagccc
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ggcacctccg gcctccgcaa gaaggtgaaa gtttttgtcc agccccatta cttgcaaaat
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gtttctggtg atgggcgtta tttctctaag gatgctatcc agatcataat aaagatgtca
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gctgcaaatg gagtaaggcg tgtctgggta ggtcagaatg gattactttc cactcctgcc
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gtgtcagctg tgatccgtga aagagttggg catgatggtc caaggcacag gagcatttat
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tctgcac
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      <210> 484
      <211> 408
      <212> DNA
      <213> Eucalyptus grandis
      <400> 484
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cgatggccag aagcccggca cctccggcct ccgcaagaag gtgaaagttt ttgtccagcc
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ccattacttg caaaattttg tgcaatcaac attctatgcc ctttcagctg agaaagtcca
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tgcaacatta ggtgaccagg tcaaagctgt ggagttggca ggttgcgatt gggttcatgt
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ccttctattc tttctgcaaa ttttgcaaca ttaggtgacc aggtcaaagc tgtggagttg
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168

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cctgtgattc agagtttgag gaagcatacc caggcattct tggattgtca tcttatggtc
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tecaaatett accattggag cacetgtgat teagagtttg aggaageata cecaqqeatt
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tggagcttca gggttcactt ttcatgtgga ggctgccaaa gacaattggc aagatctcat
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gagttaagta agattatnac tagatggatt ggcacagaag actggatcct ccacacagat
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tccatcttaa gcactgctgg aagtggcaaa tttagcagtg accgaacaat tgctcagtac
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gccaaagaaa tctggaacgt agaggggtgc tgtgtaccat gaaaagcaat ttgaaactag
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accegetttt agetteeete eetteeete teteteete ttaetttata tattgegata
                                                                       300
gaggggcaac catgctctgt aatttatgct tgtaaaacca gattcattac acaaatqcac
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tccgcctaac tgcggatgag aaataagcat ggatgtaatg atatacagtg taactttcct
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cccggataca agaccaagaa cactaatagt cttcgtctct gggaagcaaa agcttcttct
                                                                       180
caggatttca accttttcca attcaatgat ggacagtatg aatcagctgg acagttqcac
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tctcgagctg aacaaatttg tgctg
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aactttggtt gggaagtcaa cccactgccg tgatccttct ccacctttcc tctccttqaa
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cctgaagatt atatcctgca gcgatgcact acagagaaag aattgttgct tcagccgtaa
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aagttttcca ctctctgttg catctccagg atataaaaca gcacaaattt gttcagctcg
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agagtgcaac tgtccagctg attcacactg tccatcattg aattggaaaa ggttgaaatc
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cctgaagatt atatcctgca gcgatgcact acagagaaag aattgttgct tcagccgtaa
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aagttttcca ctctctgttg catctccagg atataaaaca gcacaaattt gttcagctcg
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ctcagcacat cagcactgca ggaatggagg cgagtggcac aagcaatatg aaatttqcac
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tatttgttcc aaactacaac gtctcagtag cagagattct cattcctgga agtgagctat
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tgaatggctg cctcattata ggaacattgg atggggccaa tgtggaaatc agggaagaaa
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cgcggacaag ccagacttcc atgccaagtg gacggcggca aagcagaaga acaaggagcg
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aacccacate tteggtggca aggetgetee eggttactae atggecaage taactatteg
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tgaagctttg aagcaacttg gctttgactt ggaaacactg gtggagcagg aaggagatgc
                                                                       360
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tetggaetta ceageetggg gatatggatt gegttateag tatgggttgt ttaggeaggt
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ggagacatgg attggtcaac agaaggggaa gaagctttac cttgtattaa taagtcttca
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actcatggtg atagcaacag aggcagattg cctaggataa gttctgttga tgcaatggag
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acatggattg gtcaacagaa ggggaagaag ctttaccttg tattaataag tcttcatggc
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caatacgaca tacaagataa tgcgccgaat agaggcagaa gaactgtccc ttgattcctc
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tgagatagtg ataactagta ctaggcagga gattgatgag caatggcgct tgtatgatgc
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ttttgatccg atattggaga agaagctacg agcaaggata aagcgcaatg taagctgtta
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cgatcctcga cgtcggcccg gcgctcgacg acaagaaatc gtcgctgctg ctgcgggagc
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tgaggatgtc aaagcgcact ggagtcgcca tgtccctgct ggcgctgcta ttgaagctga
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tggttatgat gaaattcgtg ctgccatcaa agaagcaaag gctgttaaag acaagcctac
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aactcccaca tettgeeggt tettcaatag agggtgttga gaagggaggt acattatcag
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tgacaattcc tctggcaaca agcctgatgt cattcttatg ggtagtggtc tgagcttgag
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cacgatgaga ttgacttcga gttcctgggg aacctgagcg gcgaccctta catcctccac
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cacgacgaga tcgacttcga gttcct
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tcttgtggac gagacaccga tccgcgtgca caccaacttg gagcaccggg gcatcccgta
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PCT/NZ99/00169

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cggatgactg ggccactcgg ggagggcttg agaagaccga ctggtccaag gcgccgttcg
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tgctttttat atgagctcgg acaaggagga agtgcgagat gaattggatt tcgagtttct
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tgatgtgccc gtacggatat tttccaacaa tgagaaaaga ggagtcccat atcctcaaac
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tcaacccatg ggcgtatact cgtcaatatg gaacgcagac gattgggcta ctcaaggggg
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catgagggta tectetteaa tetggaatge agataactgg getaeteaag gtgggegget
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gaagataaac tggagccatt ctccttttat ctccacttac agaaggttcg acatcgatgc
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ggacaggccc tctcattctt cccttactcc attacaaagg cgaatgctcc cgatgggtgc
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gacgaattcg actttgaatt tttgggg
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tacccattta accageegat gaagatetat tegageetgt ggaatgetga tgaetgggee
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accegagggg gtetggagaa aacegaetgg geeaaggege eetteatege etectacagg
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gcggcggtgg
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agtgttccga ttcgggtatt ccccaacaac gagcggctgg gagtcccata tccgaaaagc
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cageegetga gagtateete etcaatetgg aatgeageeg aetgggetae acaaggeggg
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cagtttcaca cttactccat cctctggaac tctcatcaga ttgtgttctt cgtagaccaa
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gttcctgtga gagtccacag gcacactgag gctacgagcg atgcgttccc taaagaacag
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gggatgtaca tgttttccag catt
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taacaccagc aattggtggg aagggttgag ctacagcggc ctcaaaccaa atcaagcgag
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ttcagacgaa catctattca aatggtgtgg gtggaaggga acagaggcat atcctctggt
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tegatecaac gacagagttt cacacttact etatectetg gaacgeteat cagattgtgt
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ttactgcaaa gatccagtta gatttggtac acctccagca gagtgtactg catgatgtgg
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gtctttaaac ttgacttcct acccattcca tgatcttaat tcacaaatat ttgtccactt
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gaat
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tggcgacagg gaacaacgca tttacctctg gttcgacccc accgcagatt tccattccta
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gctacttcag tgcagccatt aagttgcagg ctgggtatac tgcaggagtc aatactgcct
                                                                       180
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tgggaaatat cccgggaaga ccttatacct tacagaccaa catttatgta agagctggaa
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ggttctgcaa gggaggcagc acacaaaatt ggtggaataa gagaacatat gcttacttta
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acgctgggga tagactcaaa ctccattggg taaggaagca ttatctcgtc tatgactact
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gtaatgacaa ggtcagattc aaagtagccc ctgaggaatg caggtaccac atttaatcca
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tagcctgccg agcatttttt agtatttggt aataagacag tctggtgg
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cttcaatatg gaacgcagat gactgggcta ctcaaggtgg ccgcgtaaag accgattgga
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gccacgctcc ttttatttcc acatacacaa gtttcaacat cgatgcttgc aaatacagcc
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ctggtagttc atgtacttcg tggtgggatc agccggcgta cgcctcactt accgcaaagc
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agatcatgca actcaagtgg gtacacgaga aatacatgat ttacgattac tgcaaagatt
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cagttagatt tggtaca
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atgaacgagg gagagctgtt gaagctgaag ctcgacaatt tttctggcgc tggctttct
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tccaaggcca catacttgtt tggaaaagta ggggcgcaga ttaaactcgt tcccggcgac
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tctgcgggca cagtgactgc attttatatg tcttctgagg ggacattgca tgacgaattc
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acctttggtt tgatcccact aaggattttc accgttacag cattctctgg actccattga
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agattatatt ttttgtggat gacatcccaa taagaaagta tcgaaggacg aacccttaca
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ctttcccggc aaggcccatg tgggctgtac ggatcgattc tgggatgcat ctccttgggc
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aatggacatg gcgtgcagat tagtatggac aggcagtcag gttcgggctt cgcaacgaag
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aaacaatatt tgtttggcaa gttcgaaatg caaatcaagc ttccaccagg aaattctgcg
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ggcactgttg tggctgttta tttgtattcc aatcagccaa acagagacga gatcgacatt
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gaatttttgg gcaatgttga tggcaaggac atcatcatgc agactaatgt ttttgctaat
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ggctacgatg atcgagagca gcggatcaaa ctctggttgg atcccacagc agattttcac
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acatacacaa tottttggaa cogttaccac attgtattto tggtagatgg ct
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aacgacagag titcacactt actctatcct ctggaacgct catcagattg tgtttttcgt
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ggaccaagtt ccattgagag tccacaggca cactaaggct acacgccatg tgttccctcg
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aaagcagggg atgtacatgt tctccagcat ttggaatgga gacaactggg caacgagagg
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                                                                       303
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ccatggcctc ggctgcaaat gggaggatca aaacacgacc caatcgtcct gtgctcacag
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taataatgca agtgcaaggc actggtggga taagcccgag gcgcggactc tgacgaag
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      <210> 801
      <211> 268
      <212> DNA
      <213> Pinus radiata
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agccttatgg tcttcagacg aacatctatt caaatggtgt gggtggaagg gaacagaggc
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atatectetg gttegateea acgaeagagt tteacaetta etetateete tggaaegene
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atcagattgt gtttttcgtg gaccaagt
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     <210> 802
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      <212> DNA
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acgtattta
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tettegagee cagetgggeg acagateatg ttatgtatga gggagagetg ttgaagetta
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caggggcaca gattaagctc gttccaggtg actctgcagg cacagttact gctttttata
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gtatttacct ct
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ccctccgcaa tttcaatgct gccgctactt cttcttttga tgccgccgca gaggaggtgg
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tctacgatta ttgtgcagac accaagagat tcccccaggg accgcctccc gaatgcaaat
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aaaacctcaa teetttgaat teagagaatg aactetgaat tetacettee aaggaattet
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gattcatttc tatttaca
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PCT/NZ99/00169

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240

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tcagaactct gaacatgatg aaatagact
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cagagtgagg tatcctaaaa tgtctccaga gtgtaccana gaccgtgaca tctaatagca
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cagceteett gggatagata getatatttt tattetatte ttettegaca tatggetgtt
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gaaagtaccc aagaagaatt tcatctactt atccattgag gccactttgg gtatatggat
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      <212> DNA
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ccatggaatt tcttgtacga agatacgaac ggagcagccg cccagttggt cttctcaagg
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tttgaatttc tagggaacag aagtggacag ccttatggtc ttcagacgaa catctattca
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aatggtgtgg gtggaaggga acagaggcat atcctctggt tcgatccanc gacagagttt
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tgttttcagt ggaggaaagg gggacagaga gcaacgcgta tatctctggt ttgacccac
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tgatgtcccc atcagagttt tcaagaacag caaggattta ggagtgaggt atccattcaa
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ccagcccatg aaaatctatt caagcttgtg gaatgctgat gactgggcta caaggggtgg
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gttggagaag acagactgga gcaaggcacc ctttgttgca tcatacaagg gattccacgt
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ggatgggtgt gaggcgtcta tgcctcactc tgcttgtcca actttaggcc cgtcgatggt
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agtatgcaga taaagatggt tcctggtgac tctgcaggcg ttgtgactgc cttttattta
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ggctccagtg ggtacgaaag aactacatga tctacgatta ttgtgcagac accaagagat
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tcccccaggg accgcctccc gattgcaaat aaaacctcaa tcctttgaat tcagagaatg
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aactctgaat tctaccttcc aagtattctg attcatttct attacattaa ttctcattct
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ttctcagaca cacatgtaaa atattagagg gtatcaatca tttcattttg gtactgctat
                                                                       480
acaaaagcga gattcttttg atgaaaaaaa aaa
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aagaagaatt tcatctactt atccattgag gccactttgg gtatatggat caatatggga
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gcagctcttg cttctgcaaa tttctacaat gatgtcgaca ttacatgggg taatgatcgt
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gctaaaatca ttgacaatgg acaagagttg cagcttactc ttgaccgctc ttcaggttgt
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ggtattcaat ccaagcaaga gtatctattt gccaagattg atatccaaat caagttggta
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cctggcaact ctgcaggcac agtcactacc ttttatctat catctcaagg tcccaaacac
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tgtggttcga cccaaccttg gatttccaca cttactccgt gctctggaca tcaaaccaaa
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tcatattctc tgtagacgag actcccgttc gagtgtttaa gaacagggag acagagttgg
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gtaaagtgga tagcaattat cactateeta agagecaage aatgaaggte tatteaagee
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tctggaatgc agatgattgg gcgactagag gtggactcgt caagacagac t
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      <212> DNA
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aatggccaag tatggcacct ggttcttgac cagaactcag gttctgggtt caagtccaag
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tataagtaca gattcggatg gtttagcatg aagctcaagc tcgtaccggg agactctgca
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ggagttgtca ctgcttatta tatgtcttct aacaccgaca tgaataggga cgagctggac
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gaaagggaac cttatcccca ggttcttgca gttcttgaac acgcggattg gtaccgagtc
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cacaaaaaaa ctgcacaaaa aacccatcac acacatcaat attcatgaac gttccagtgc
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caaattttga aaagtttttt tggtttttta ggattttatt tgtttagaat tttggaagga
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ttgtgaattt ttcagaataa aaatatttaa aaaattttca aatatct
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ctacaattac tgcactgaca cgcccagaaa caagcaaatg cctccggaat gtgttcgcga
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tcgcgacaat atgtagtcca gttatcctca tcatttgatg ctacccatgg ctgaataatc
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cqtqqtcqqa taat
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ggcaactctg caggcacagt cactactttt tatctatcat ctcaaggtcc caaacacgac
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gaaatagact ttgaatttct gggaaacctg tctggagatc cttatatttt gcacactaat
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gaatat
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999
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      <212> DNA
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      <400> 859
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      <210> 860
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      <212> DNA
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ccaccaagga ttaccattcc tatgctgtgc tctggaacat gtaccaaatt gcatttttgg
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tagatgaggt accaatccgg gtgttcaaga acagcaagga tctgggcgtg aggtacccat
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ttaaccagcc gatgaagatc tattcgagcc tgtggaatgc tgatgactgg gccacccgag
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acgtcgatgc ctgtga
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gggcacgacg aaattgatat ggagttccta ggaaatgttt ctggggagcc ctacattctg
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      <212> DNA
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tagatgaggt accaatcegg gtgttcaaga acagcaagga tetgggegtg aggtacceat
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      <212> DNA
      <213> Pinus radiata
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